



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 138939

TO: Terra Gibbs
Location: rem/2d10/2c18
Art Unit: 1635
Tuesday, December 07, 2004

Case Serial Number: 09/491063

From: Peggy Ruppel
Location: Biotech-Chem Library
REMSSEN 1B65
Phone: 571-272-2557

Peggy.Ruppel@uspto.gov

Search Notes

The results of your sequence search request are attached. Please contact me if you have any questions or comments.

Thank you for using STIC services.

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STIC-Biotech/ChemLib

138939

my

From: Gibbs, Terra
Sent: Tuesday, November 30, 2004 10:11 AM
To: STIC-Biotech/ChemLib
Subject: Sequence search request...

Could you please do a regular search of SEQ ID NO:1 of USSN 09/491063 in all commercial and pending databases?
Could you please do a regular search of SEQ ID NO:2 of USSN 09/491063 in all commercial and pending databases?

Terra Cotta Gibbs, Ph.D.
Art Unit 1635
Remsen Building 2D10
Mailbox 2C18
571-272-0758

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(STIC)

STAFF USE ONLY

Searcher: _____
Searcher Phone: 2- _____
Date Searcher Picked up: _____
Date Completed: _____
Searcher Prep/Rev. Time: _____
Online Time: _____

Type of Search

NA Sequence: # _____
AA Sequence: # _____
Structure: # _____
Bibliographic: _____
Litigation: _____
Patent Family: _____
Other: _____

Vendors and cost where applicable

STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

is Page Blank (uspto)

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2004, 10:17:04 ; Search time 4769 Seconds
(without alignments)
10739.095 Million cell updates/sec

Title: US-09-491-063a-1
Perfect score: 1083
Sequence: 1 atgcccccccaagaatt.....gcaatcagaagcgcgaggt 1083

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenBml:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_srs:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1076	99.4	2601	14 TMWALR	L14460 Tomato mot
2	1047.8	96.7	1086	14 TMWREPRO	M90495 Tomato mot
3	1047.8	96.7	1162	6 AR170763	AR170763 Sequence
4	1044.6	96.5	1169	6 AR170765	AR170765 Sequence
5	1043	96.3	1169	6 AR170766	AR170766 Sequence
C 6	1040.8	96.1	2602	6 AR170774	AR170774 Sequence
7	1039.8	96.0	1169	6 AR170764	AR170764 Sequence
8	1033.8	95.5	1166	6 AR170771	AR170771 Sequence
C 9	905.6	83.6	2642	14 AF049336	AF049336 Sida gold
C 10	856.4	79.1	2632	14 GEABMVA	X15983 Abutilon mo
C 11	840.4	77.6	2634	14 AM051137	AM051137 Abutilon mo
C 12	825.4	76.2	2634	14 AF010476	AF010476 Chino del
C 13	825	76.2	2155	14 TM056319	TM056319 Tomato mo
C 14	821.8	75.9	2597	14 AF012300	AF012300 Tomato mo
C 15	817.4	75.5	2635	14 AF226664	AF226664 Chino del
C 16	814.2	75.2	2635	14 AF226665	AF226665 Chino del
C 17	809.8	74.8	2612	14 SGWV2612	Y11099 Sida yellow
C 18	806	74.4	2190	14 TLE488768	AJ488768 Tobacco 1
C 19	773.2	71.4	2615	14 BDMARAL13A	M88179 Bean dwarf

C 20	771.4	71.2	2603	14 SGWV2603	Y11097 Sida golden
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C 23	761.6	70.3	2601	14 SG0577395	X59550 Sida gold
C 24	759.2	70.1	2605	14 SGWVAVAC	X99550 Sida golden
C 25	757.6	70.0	2620	14 HTVDANCA	Y14874 Tomato mosa
C 26	710.6	65.6	2584	14 TICVY15034	Y15034 Potato yell
C 27	704.8	65.1	2593	14 PYVVA	D00940 Potato yell
C 28	704.2	65.0	2644	14 BG0544531	AJ544531 Bean gold
C 29	702.2	64.8	2644	14 AR170772	AR170772 Sequence
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C 40	689.6	63.7	1062	6 AR170803	AR170803 Sequence
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C 43	680.6	62.8	2647	6 E00867	E00867 DNA encodin
C 44	680.6	62.8	2647	6 E01003	E01003 Vector DNA
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ALIGNMENTS

RESULT 1
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LOCUS Tomato mottle virus-[Florida] complete A component DNA; coat
DEFINITION protein (AR1), replicative protein (AR1), transcriptional element
(AL2), and AL3 genes, complete cds.

ACCESSION L14460
VERSION L14460.1 GI:295320
KEYWORDS Tomato mottle virus-[Florida]
SOURCE Tomato mottle virus-[Florida]
ORGANISM
REFERENCE 1 (bases 1 to 2601)
AUTHORS Abouzid,A.M., Poleton,J.E. and Hiebert,E.
TITLE The nucleotide sequence of tomato mottle virus, a new geminivirus
isolated from tomatoes in Florida
JOURNAL J. Gen. Virol. 73 (Pt 12), 3225-3229 (1992)
MEDLINE 93107858
PubMed 1469361

FEATURES

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99.4%; Score 1076; DB 14; Length 2601;
Best Local Similarity 100.0%; Pred. No. 6e-301;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

ORIGIN
Query Match 99.4%; Score 1076; DB 14; Length 2601;
Best Local Similarity 100.0%; Pred. No. 6e-301;
Matches 1076; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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2601 CACCAAGAAATTTAGAGTTCACTCAAGAACTATTTCTTAATCCCAAGTCTCTC 2542
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2541 TATCTAAGAGAGCACTTCCCAATTAAGAACTTAATACCCCAAGTCAAGAAAT 2482
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2421 AGTTGGAAGTTAGTACCAATGACGAAATTAACAGATTCTTGACCTGGTCTCCCAACC 2362
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368 CCAAGAGAGCGCAGAGTCTGCTAATGATTCATATGCAAAAGCATTAATGAGGTTGG 427
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2241 CCAAGAGAGCGCAGAGTCTGCTAATGATTCATATGCAAAAGCATTAATGAGGTTGG 2182
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DB 2061 CATTTCAGTCTCTCTTTTCACTAAGCTTCTGACGAGATGCAAGATGGCCGATTAAT 2002
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QY 608 ATTTCGGGACGGGAGACGCTGCCGCCGAGATAGACCTGTAAATGATCATGCTCGAGGATG 667
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DB 2001 ATTTCGGGACGGGAGACGCTGCCGCCGAGATAGACCTGTAAATGATCATGCTCGAGGATG 1942
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QY 668 ATTCAAGACAGGAGACGATGAGGAGCGGTGAGGCTTAAGCCCATTAATCTATCTAGTG 727
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DB 1941 ATTCAAGACAGGAGACGATGAGGAGCGGTGAGGCTTAAGCCCATTAATCTATCTAGTG 1882
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QY 728 GACACCTAGACTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 787
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DB 1881 GACACCTAGACTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1822
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QY 788 ACATCGACCGCATTTATCTAAGGATTAAGCACTGAAAGAAATGCTGGGGCCGAGAAAG 847
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RESULT 2
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LOCUS Tomato mottle virus replicative protein (AL1) gene, complete cds.
DEFINITION M90495
ACCESSION M90495.1 GI:335252
VERSION 1
KEYWORDS
SOURCE
ORGANISM
Tomato mottle virus
Virus; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE
1 (sites)
Gibbertson, R.L., Hidayat, S.H., Rojas, M.R. and Maxwell, D.P.
Infectious DNA clones of a new geminivirus associated with tomatoes
in Florida
Phytopathol. 81, 1184-1184 (1991)
2 (bases 1 to 1086)
Hou, Y.M. and Maxwell, D.P.
Pseudorecombination between infectious cloned DNA components of
Tomato mottle and bean dwarf mosaic geminiviruses
JOURNAL J. Gen. Virol. 74 (Pt 1), 23-31 (1993)
MEDLINE 93139780
PUBMED 8423448
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Location/Qualifiers
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ORIGIN

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Query Match      96.7%; Score 1047.8; DB 14; Length 1086;
Best Local Similarity 98.0%; Pred. No. 8.8e-293;
Matches 1061; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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RESULT 3
AR170763
LOCUS AR170763 1162 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 1 from patent US 6291743.
ACCESSION AR170763
VERSION AR170763.1 GI:17908722
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1162)
AUTHORS Stout,J.T., Liu,H.T., Hanson,S.F., Maxwell,D.P., Ahlquist,P.G. and
Gilbertson,R.L.
TITLE Transgenic plants expressing mutant geminivirus AC1 or CI genes
JOURNAL Patent: US 6291743-A 1 18-SBP-2001;
FEATURES
location/Qualifiers
source 1..1162
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ORIGIN

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Query Match      96.7%; Score 1047.8; DB 6; Length 1162;
Best Local Similarity 98.0%; Pred. No. 8.8e-293;
Matches 1061; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTAATTTCCCGAG 60
DB 44 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTAATTTCCCGAG 103
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DB 104 TGGCTCTATCTAAGAAAGACATTTCCCAATTAACAAACCTAAATCCCGATCAAC 163
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DB 224 CTGTGTCAGTTCAGAGTAAGTACCAATGCAAGATTAACAGATTTCTTGAACCTGATCTCC 283
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QY	421	GGTTCGGTTCATCTGCGCTTAGCGGTTCTAAGGAAAGAACCAAAAGATTTGTATTA	480
Db	464	AGTTCGGTTCATCTGCGCTTAGCGGTTCTAAGGAAAGAACCAAAAGATTTGTATTA	523
QY	481	CAAAATCATACATCCGCTCTTAACCTAGAACGAATATTGCGAAAAGCTCCGGAACCGTGG	540
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Db	704	GAGGCTGATTCAGAAACAGGGAAGACGATGTGGGCGCGTGCCTTAGCGCCACATPACTAT	763
QY	721	CTCAGTGGACACCTAGACTTCAATAGTGTGAGATCTTCTGAAATGATGTGCAATATPAAGTGC	780
Db	764	CTCAGTGGACACCTAGACTTCAATAGTGTGAGATCTTCTGAAATGATGTGCAATATPAAGTGC	823
QY	781	ATTGATGACATCGACCGCATTTATCTTAAAGCTAAAGCACTGGAAGAAATTTGCTGGGGCC	840
Db	824	ATTGATGACATCGACCGCATTTATCTTAAAGCTAAAGCACTGGAAGAAATTTGCTGGGGCC	883
QY	841	CAGAAAGTTTGGCAATCAAAATTGCAAGTACGCTAAGCCAGTTCAAATTAAGGGGGAATC	900
Db	884	CAGAAAGTTTGGCAATCAAAATTGCAAGTACGCTAAGCCAGTTCAAATTAAGGGGGAATC	943
QY	901	CCAGCAATTCGTGCTTTCGAATCTCGTGTAGGGGTGCAGCTTAAAGATTTCTTAGACAAA	960
Db	944	CCAGCAATTCGTGCTTTCGAATCTCGTGTAGGGGTGCAGCTTAAAGATTTCTTAGACAAA	1003
QY	961	GCAAGAAATACAGGCTCTCAAGAACCTGACGTAATCAAGAAATGCGATCTTCATCACTCTACA	1020
Db	1004	GCAAGAAATACAGGCTCTCAAGAACCTGACGTAATCAAGAAATGCGATCTTCATCACTCTACA	1063
QY	1021	GCCCCCCTCTATCAAGAGAGACACAGGCAAGCCAAAGAAAGGGGCAATCAGAGGCGGAG	1080
Db	1064	GCCCCCCTCTATCAAGAGAGACACAGGCAAGCCAAAGAAAGGGGCAATCAGAGGCGGAG	1123
QY	1081	GGT 1083	
Db	1124	GGT 1126	
RESULT 4			
ARI170765			
LOCUS	ARI170765	1169 bp	DNA linear PAT 17-DEC-2001
DEFINITION	Sequence 5 from patent US 6291743.		
ACCESSION	ARI170765		
VERSION	ARI170765.1	GI:17908724	
KEYWORDS			
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1169)		
	Stout,J.T., Luu,H.T., Hanson,S.F., Maxwell,D.P., Ahlquist,P.G. and		
	Gilbertson,R.L.		
	Transgenic plants expressing mutant geminivirus AC1 or CI genes		
	Patent: US 6291743-A 5 18-SEP-2001;		
	Location/Qualifiers		
TITLE	Transgenic plants expressing mutant geminivirus AC1 or CI genes		
JOURNAL	Patent: US 6291743-A 5 18-SEP-2001;		
FEATURES	Location/Qualifiers		

ORIGIN	source	1..1169	/organism="unknown"	/mol_type="unassigned DNA"
Query Match	96.5%;	Score 1044.6;	DB 6;	Length 1169;
Best Local Similarity	97.8%;	Pred. No. 7.5e-292;		
Matches 1059;	Conservative	0;	Mismatches 24;	Indels 0; Gaps 0;
OY	1	ATGCCCCCAACAAAGAAATTTAGATTGAGTTTCAGTCAAAAGAACTATTTCCTACTTATCCCGAC	60	
DB	44	ATGCCCCCAACAAAGAAATTTAGATTGAGTTTCAGTCAAAAGAACTATTTCCTACTTATCCCGAC	103	
OY	61	TGCTCTCATTTAAGAAAGAGCACTTCCCAATTAACAAACCTTAATACCCAGTCAAC	120	
DB	104	TGCTCTTTGTTTAAAGAAAGAGCACTTCCCAATTAACAAACCTTAATACCCAGTCAAT	163	
OY	121	AAGAAATTCATCAAAATTTTGAGAGAGCTTCATGAAAATGGGGAACCTCATCTTCATGTG	180	
DB	164	AAGAAATTCATCAAAATTTTGAGAGAGCTTCATGAAAATGGGGAACCTCATCTTCATGTG	223	
OY	181	CTGTGTGAGTTCCAAAGTAAAGTACCAATTCACCAATTAACAGATTCTTCGACCTGCTCC	240	
DB	224	CTGTGTGAGTTCCAAAGTAAAGTACCAATTCACCAATTAACAGATTCTTCGACCTGCTCC	283	
OY	241	CCAACCCGGTCAGACATTCCTCAGCAATATTACGAGAGCTAAATGAGCTCCGACGTC	300	
DB	284	CCAACCCGGTCAGACATTCCTCAGCAATATTACGAGAGCTAAATGAGCTCCGACGTC	343	
OY	301	AAATCATACATCGAACAGAGCGAGATACAAATCGAATGGGAGATTTCCAAATGCAGGC	360	
DB	344	AAATCGTACATCGAACAGAGCGAGATACAAATCGAATGGGAGATTTCCAGATCGAGGC	403	
OY	361	AGATCTCCAGAGAGGCGCAGCACTCTGCTTAATGATTCATATGCGAAGACATTTAAATGCA	420	
DB	404	AGATCTCCAGAGAGGCGCAGCACTCTGCTTAATGATTCATATGCGAAGACATTTAAATGCA	463	
OY	421	GGTTCGGTTCATCTGCTTACAGCGTTCTTAAGGGAACCAACCAAAAGATTTTGATTA	480	
DB	464	AGTTCGGTTCATCTGCTTACAGCGTTCTTAAGGGAACCAACCAAAAGATTTTGATTA	523	
OY	481	CAAAATCATACATCGCTCTTAACCTTAAGAACGAATATTTCCAAAGGCTCCGGAACGCTGG	540	
DB	524	CAAAATCATACATCGCTCTTAACCTTAAGAACGAATATTTCCAAAGGCTCCGGAACGCTGG	583	
OY	541	GTTCCTCATTTCAAGTCTCTTTTCACTAAGCTTCCTGACGAGATGCGAATGGGGCG	600	
DB	584	GTTCCTCATTTCAAGTCTCTTTTCACTAAGCTTCCTGACGAGATGCGAATGGGGCG	643	
OY	601	GATAAATTAATTCGAGAGCGGTTGACGCTGCGCGCGGATAGACTGTAAATCATCGTC	660	
DB	644	GATAAATTAATTCGAGAGCGGTTGACGCTGCGCGCGGATAGACTGTAAATCATCGTC	703	
OY	661	GAGGTTAATTCAGAACAGGAGACGATGTGGGCGGTGGCTTAAGGCCCAATACATAT	720	
DB	704	GAGGTTAATTCAGAACAGGAGACGATGTGGGCGGTGGCTTAAGGCCCAATACATAT	763	
OY	721	CTCAGTGGACCTTAAGCTTCAATGCTGAGTCTTTCGAAATGATGAGATTAAGTCAAGTC	780	
DB	764	CTCAGTGGACCTTAAGCTTCAATGCTGAGTCTTTCGAAATGATGAGATTAAGTCAAGTC	823	
OY	781	ATTATGATCATTCGACCGCATTTATCTTAAGCTTAAGACCTGGAAGAAATTTCTGGGGGCC	840	
DB	824	ATTATGATCATTCGACCGCATTTATCTTAAGCTTAAGACCTGGAAGAAATTTCTGGGGGCC	883	
OY	841	CAGAAAGATTGGCAATCAAAATTCGAGTACCGGTAAGCCAGTTCAAAATTTAAAGCGGGAATC	900	
DB	884	CAGAAAGATTGGCAATCAAAATTCGAGTACCGGTAAGCCAGTTCAAAATTTAAAGCGGGAATC	943	
OY	901	CCAGCAATTCGGCTTTGCAATCCGCTGAGAGGGTCCAGCTAATTAAGATTTTGAACAA	960	
DB	944	CCAGCAATTCGGCTTTGCAATCCGCTGAGAGGGTCCAGCTAATTAAGATTTTGAACAA	1003	

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QY 961 GCAGAAATACAGCTCTCAAGAACTGACTATCAAGATCGATCTTCAATCACTCCACCA 1020
DB 1004 GCAGAAATACAGCTCTCAAGAACTGACTATCAAGATCGATCTTCAATCACTCCACCA 1063
QY 1021 GCGCCCTCTATCAAGAGCAGACAGGCGGCAAGAAACGGGCAATCAAGAGGGCGAG 1080
DB 1064 GCGCCCTCTATCAAGAGCAGACAGGCGGCAAGAAACGGGCAATCAAGAGGGCGAG 1123
QY 1081 GGT 1083
DB 1124 GGT 1126

RESULT 5
ARI70766 1169 bp DNA linear PAT 17-DEC-2001
LOCUS Sequence 7 from patent US 6291743.
DEFINITION ARI70766
ACCESSION ARI70766
VERSION ARI70766.1 GI:17908725
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1169)
AUTHORS Stout,J.T., Luu,H.T., Hanson,S.F., Maxwell,D.P., Ahlquist,P.G. and
Gilbertson,R.L.
TITLE Transgenic plants expressing mutant geminivirus AC1 or CI genes
JOURNAL Patent: US 6291743-A 7 18-SEP-2001;
FEATURES
source 1..1169
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 96.3%; Score 1043; DB 6; Length 1169;
Best Local Similarity 97.7%; Pred. No. 2.2e-291;
Matches 1058; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

QY 1 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTCACTTATCCCAAG 60
DB 44 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTCACTTATCCCAAG 103
QY 61 TGTCTCTATCTAAAGAGACATTTCCCAATTACAAAACCTAAATACCCAGTCAAC 120
DB 104 TGTCTCTATCTAAAGAGACATTTCCCAATTACAAAACCTAAATACCCAGTCAAT 163
QY 121 AAGAAATTCATCAAAATTTGCAGAGAGCTTCATGAATAATGGGAACTCTCATCTCATGTG 180
DB 164 AAGAAATTCATCAAAATTTGCAGAGAGCTTCATGAATAATGGGAACTCTCATCTCATGTG 223
QY 181 CTGTTCAGTTCGAGGTAAGTACCAATGACGAAATTAAGATTTCTTCACTTCTCC 240
DB 224 CTGTTCAGTTCGAGGTAAGTACCAATGACGAAATTAAGATTTCTTCACTTCTCC 283
QY 241 CCAACCCGGTACAGCATTTTCCATTCGAATTTCAAGGAGCTTAATTCAGACTCCGAGCTC 300
DB 284 CCAACCCGGTACAGCATTTTCCATTCGAATTTCAAGGAGCTTAATTCAGACTCCGAGCTC 343
QY 301 AATTCATCATCGACAGAGAGATATCAATGAATGGGAGATTTCCAAATCGACGGC 360
DB 344 AATTCATCATCGACAGAGAGATATCAATGAATGGGAGATTTCCAAATCGACGGC 403
QY 361 AGATCTGCCAGAGAGGCCAGAGTCTGTAATGATTCATATGCGAAAGCATTTAAATGCA 420
DB 404 AGATCTGCCAGAGAGGCCAGAGTCTGTAATGATTCATATGCGAAAGCGTTAAATGCA 463
QY 421 GGTTCGGTCAATCTGCTTAAGGGTCTTAAGGGAAGAAACAACCAAAAGATTTTGTATTA 480
DB 464 AGTTCGGTCAATCTGCTTAAGGGTCTTAAGGGAAGAAACAACCAAAAGATTTTGTATTA 523
QY 481 CAATAATCATACATCGCTCTAATCCTAGACGAATATTTGCAAAAGGCTCGGAACCGTGG 540
DB 524 CAATAATCATACATCGCTCTAATCCTAGACGAATATTTGCAAAAGGCTCGGAACCGTGG 583

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QY 541 GTTCTTCATTTCAAGTCTCTTCTTCACTAAAGTTTCTGACGAGATGACAGAAATGGCG 600
DB 584 GTTCTTCATTTCAAGTCTCTTCTTCACTAAAGTTTCTGACGAGATGACAGAAATGGCG 643
QY 601 GATTAATTTTGGGACGGGTGACGTGGCGCGCGGCAATAGACCTTATGATTCATCGTC 660
DB 644 GATTAATTTTGGGACGGGTGACGTGGCGCGCGGCAATAGACCTTATGATTCATCGTC 703
QY 661 GAGGTGATTTCAAGAACAGGAGAGACGATGGGCGCGTGGCTTAGGCCACATTAATAT 720
DB 704 GAGGTGATTTCAAGAACAGGAGAGACGATGGGCGCGTGGCTTAGGCCACATTAATAT 763
QY 721 CTCAGTGAACCTTAGACTTCAATGCTCGAGTCTTCTGAAATGATGCAATTAACGTC 780
DB 764 CTCAGTGAACCTTAGACTTCAATGCTCGAGTCTTCTGAAATGATGCAATTAACGTC 823
QY 781 ATTGAATGATGCAACCGGATTAATGCTTAAGCACTGGAAGAAATTTGCTGAGGGCC 840
DB 824 ATTGAATGATGCAACCGGATTAATGCTTAAGCACTGGAAGAAATTTGCTGAGGGCC 883
QY 841 CAGAAATTTGGCAATCAATTTGCAAGTACGGTAAAGCCAGTTCAATTAAGCGGCAATC 900
DB 884 CAGAAATTTGGCAATCAATTTGCAAGTACGGTAAAGCCAGTTCAATTAAGCGGCAATC 943
QY 901 CCAGCAATCGTCTTTCGATTCATCTGAGGGTCCAGCTATTAAGAGTTCTTACACAA 960
DB 944 CCAGCAATCGTCTTTCGATTCATCTGAGGGTCCAGCTATTAAGAGTTCTTACACAA 1003
QY 961 GCAGAAATACAGCTCTCAAGAACTGACTATCAAGATCGATCTTCACTTATCCCAAG 1020
DB 1004 GCAGAAATACAGCTCTCAAGAACTGACTATCAAGATCGATCTTCACTTATCCCAAG 1063
QY 1021 GCGCCCTCTATCAAGAGCAGACAGGCGGCAAGAAACGGGCAATCAAGAGGGCGAG 1080
DB 1064 GCGCCCTCTATCAAGAGCAGACAGGCGGCAAGAAACGGGCAATCAAGAGGGCGAG 1123
QY 1081 GGT 1083
DB 1124 GGT 1126

RESULT 6
ARI70774/c 2602 bp DNA linear PAT 17-DEC-2001
LOCUS ARI70774
DEFINITION Sequence 17 from patent US 6291743.
ACCESSION ARI70774
VERSION ARI70774.1 GI:17908733
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2602)
AUTHORS Stout,J.T., Luu,H.T., Hanson,S.F., Maxwell,D.P., Ahlquist,P.G. and
Gilbertson,R.L.
TITLE Transgenic plants expressing mutant geminivirus AC1 or CI genes
JOURNAL Patent: US 6291743-A 17 18-SEP-2001;
FEATURES
source 1..2602
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 96.1%; Score 1040.8; DB 6; Length 2602;
Best Local Similarity 98.0%; Pred. No. 1e-290;
Matches 1054; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 8 CACCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTAATTTCCCAAGTGTCTC 67
DB 2602 CACCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTAATTTCCCAAGTGTCTC 2543
QY 68 TATCTAAGAGAGACCTTCCCAATTCAAACCTAATATCCCAAGTCAACAGAAAT 127

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Db 2542 TGTCTAAGAGAGCACTTCCCAATTACAAAACCTAATATCCCAAGTCAATAAGAAAT 2483
Qy 128 TCATCAAAATTTGCGAGAGAGCTTCATGAAATGGGAAACCTCATCTCATGTGCTTGTTC 187
Db 2482 TCATCAAAATTTGCGAGAGAGCTTCATGAAATGGGAAACCTCATCTCATGTGCTTGTTC 2423
Qy 188 AGTTCGAAGGTAGTACCAATGACGAATTAACAGATTTTGACCTGGTCTCCCAACCC 247
Db 2422 AGTTCGAAGGAAGTACCAATGACGAATTAACAGATTTTGACCTGGTCTCCCAACCC 2363
Qy 248 GGTGAGACATTTTCATCCGAATATTCAGGAGCTTAATGAGCTCCGACGTCATTAATCAT 307
Db 2362 GGTGAGACATTTTCATCCGAATATTCAGGAGCTTAATGAGCTCCGACGTCATTAATCAT 2303
Qy 308 ACATCGACGAAGGAGGAGATCAATCGAATGGGAGATTTCCAAATCGACGGCAGATCTG 367
Db 2302 ACATCGACGAAGGAGGAGATCAATCGAATGGGAGATTTCCAAATCGACGGCAGATCTG 2243
Qy 368 CCAAGGAGGCGCAGAGCTCTGCTAATGATATGCAAAAGCATTTAAATGAGGTTCCG 427
Db 2242 CCAAGGAGGCGCAGAGCTCTGCTAATGATATGCAAAAGCATTTAAATGAGGTTCCG 2183
Qy 428 TTCAATCTGCTTAAAGGCTTAAAGGAAACAACCAAAAGATTTGTATTACAAATC 487
Db 2182 TTCAATCTGCTTAAAGGCTTAAAGGAAACAACCAAAAGATTTGTATTACAAATC 2123
Qy 488 ATAAATCCGCTTAACCTAAGCAATTCGAAAGGCTCCGAAACCGTGGTCTC 547
Db 2122 ATAAATCCGCTTAACCTAAGCAATTCGAAAGGCTCCGAAACCGTGGTCTC 2063
Qy 548 CATTTCAAGTCTCTTCTTCACTAAGCTTCTGACGAGATCGAGAAATGGCGGATTAAT 607
Db 2062 CATTTCAAGTCTCTTCTTCACTAAGCTTCTGACGAGATCGAGAAATGGCGGATTAAT 2003
Qy 608 ATTTGCGGAGCGGTTGACGCTCCGCGCGCGATTAAGCTGTAATCATCTGTCAGAGGTG 667
Db 2002 ATTTGCGGAGCGGTTGACGCTCCGCGCGCGATTAAGCTGTAATCATCTGTCAGAGGTG 1943
Qy 668 ATTCAGAAACGAGGAAGCAATGGGCGGTGGTTAAGGCCCATTAATCATCTGTCAGGTG 727
Db 1942 ATTCAGAAACGAGGAAGCAATGGGCGGTGGTTAAGGCCCATTAATCATCTGTCAGGTG 1883
Qy 728 GACACCTAGACTTCAATGTCGAGTCTTCTGAAATGATGTCAGATTAACCTCATTTGATG 787
Db 1882 GACACCTAGACTTCAATGTCGAGTCTTCTGAAATGATGTCAGATTAACCTCATTTGATG 1823
Qy 788 ACATCGCACCGCATTTATCTAAAGCTAAAGCACTGGAAGAAATGCTGGGGGCCGAAAG 847
Db 1822 ACATCGCACCGCATTTATCTAAAGCTAAAGCACTGGAAGAAATGCTGGGGGCCGAAAG 1763
Qy 848 ATTCGCAATCAAAATTTGACAGTACGTAAGCAATTAAGGAGGGAATCCAGCA 907
Db 1762 ATTCGCAATCAAAATTTGACAGTACGTAAGCAATTAAGGAGGGAATCCAGCA 1703
Qy 908 TCGTCTTTGCAATCTGTCGAGGAGTGCACGCTAATAAGATTTTGAACAAGCAGAAA 967
Db 1702 TCGTCTTTGCAATCTGTCGAGGAGTGCACGCTAATAAGATTTTGAACAAGCAGAAA 1643
Qy 968 ATACAGGCTCTAAGAACTGAGCTATCAAGAAATGAGATTTTATCACTCAGACCCGCC 1027
Db 1642 ATACAGGCTCTAAGAACTGAGCTATCAAGAAATGAGATTTTATCACTCAGACCCGCC 1583
Qy 1028 TCTATCAGAGAGCACAGGCAAGCCAAAGAAAGGCGCAATCAGAAAGCGCGAGGT 1083
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RESULT 7
LOCUS ARI70764 1169 bp DNA linear PAT 17-DEC-2001
DEFINITION Sequence 3 from patent US 6291743.
ACCESSION ARI70764
VERSION ARI70764.1 GI:17908723

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KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1169)
AUTHORS Scout, J. T., Luu, H. T., Hanson, S. F., Maxwell, D. P., Ahlquist, P. G. and
Gillbertson, R. L.
TITLE Transgenic plants expressing mutant geminivirus AC1 or CI genes
JOURNAL Patent: US 6291743-A 3 18-SEP-2001;
FEATURES
source Location/Qualifiers
1..1169
/organism="unknown"
/mol_type="unassigned DNA"

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ORIGIN
Query Match 96.0%; Score 1039.8; DB 6; Length 1169;
Best Local Similarly 97.5%; Pred. No. 1,39e-290;
Matches 1056; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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Qy 1 ATGCCCCACCAAGAAATTTAGAGTTCAGTCAAGAACTATTCTTACTTATCCAG 60
Db 44 ATGCCCCACCAAGAAATTTAGAGTTCAGTCAAGAACTATTCTTACTTATCCAG 103
Qy 61 TGTCTCTATCTAAGAAAGAGACATTTCCCAATTACAAAACCTAATACCCAGTCAC 120
Db 104 TGTCTCTTGTCTAAGAAAGAGACATTTCCCAATTACAAAACCTAATACCCAGTCAT 163
Qy 121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAGAAATGGGAACTCATCTCATGTG 180
Db 164 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAGAAATGGGAACTCATCTCATGTG 223
Qy 181 CTGTTGAGTTCGAAGTAAAGTAACTCAATGACGAATTAAGATTTCTGACCTGCTCC 240
Db 224 CTGTTGAGTTCGAAGTAAAGTAACTCAATGACGAATTAAGATTTCTGACCTGCTCC 283
Qy 241 CCAACCCGATCAGACATTTTCATCCGAATATTCAAGGAGCTAATTCAGCTCCGAGTC 300
Db 284 CCAACCCGATCAGACATTTTCATCCGAATATTCAAGGAGCTAATTCAGCTCCGAGTC 343
Qy 301 AATCATATCATCGACAAAGACGAGATGATGAATGGGAAATTTCCAAATCGACGCC 360
Db 344 AATCATATCATCGACAAAGACGAGATGATGAATGGGAAATTTCCAAATCGACGCC 403
Qy 361 AGATCTGCGAGAGGCGCAGAGTCTGTAATGATTCATATGCGAAAGCATTAATGCA 420
Db 404 AGATCTGCGAGAGGCGCAGAGTCTGTAATGATTCATATGCGAAAGCATTAATGCA 463
Qy 421 GGTTCGGTTCATCTGCTTAAAGCGGTTCTAAGGAAAGCAACCAAAAGATTTGATTA 480
Db 464 GGTTCGGTTCATCTGCTTAAAGCGGTTCTAAGGAAAGCAACCAAAAGATTTGATTA 523
Qy 481 CAAATATATTAACATCCGCTCTTAACCTTAAGCAATATTCGCAAAAGCTCCGGAACCGTGG 540
Db 524 CAAATATATTAACATCCGCTCTTAACCTTAAGCAATATTCGCAAAAGCTCCGGAACCGTGG 583
Qy 541 GTTCCTCATTTTAAAGTCTCTTCTTCACTAAGGTTCTGACGAGATGACGAATGGGCG 600
Db 584 GTTCCTCATTTTAAAGTCTCTTCTTCACTAAGGTTCTGACGAGATGACGAATGGGCG 643
Qy 601 GATTAATTAATTTGCGAGCGGTTGACGCTGCGCGCGCGAGTACCTGTAATGATCATGTC 660
Db 644 GATTAATTAATTTGCGAGCGGTTGACGCTGCGCGCGCGAGTACCTGTAATGATCATGTC 703
Qy 661 GAGGTGATTCAGAAACAGGGAAGACGATGTGGGCGGTGCTTAAGGCCCACTAATAT 720
Db 704 GAGGTGATTCAGAAACAGGGAAGACGATGTGGGCGGTGCTTAAGGCCCACTAATAT 763
Qy 721 CTGAGTGAACCTTGAAGCTTCATGTCGAGTCTTCTGATGATGTCAGTAAAGTCTC 780
Db 764 CTGAGTGAACCTTGAAGCTTCATGTCGAGTCTTCTGATGATGTCAGTAAAGTCTC 823
Qy 781 ATTGATGATTCGACCGCATTTATCTAAGCTAAGCACTGGAAGATTTGCTGGGGGCC 840

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Db 824 ATTTAAATACATGCGACCGCTTATCTAAAGCTTAAAGCATGCGAAGAAATTCCTAGGGCC 883
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Db 884 CAGAAAGATTGGCAATCAATTGCAAGTACGCTAGCGCACTTCAATTAAGCGGAAATC 943
QY 901 CCAGCAATGCTGCTTTGCAATCTCTGGTAGGGGTCCAGCTATTAAGAGTTCTTAGACAA 960
Db 944 CCAGCAATGCTGCTTTGCAATCTCTGGTAGGGGTCCAGCTATTAAGAGTTCTTAGACAA 1003
QY 961 GCAGAAATACAGGCTCTCAAGAACTGACATCAAGATGCGATCTTCAATCAACCTGACA 1020
Db 1004 GCAGAAATACAGGCTCTTAAGAACTGACATCAAGATGCGATCTTCAATCAACCTGACA 1063
QY 1021 GCCCCCTCTATCAGAGACACACAGCGCAAGCAAGAAACGGGCAATCAGAAAGCGCAG 1080
Db 1064 GCGCCCTCTATCAAGACACACAGCGCAAGCAAGAAACGGGCAATCAGAAAGCGCAG 1123
QY 1081 GGT 1083
Db 1124 GGT 1126

RESULT 8
ARI70771 1166 bp DNA linear PAT 17-DEC-2001
LOCUS ARI70771 Sequence 13 from patent US 6291743.
DEFINITION ARI70771
ACCESSION ARI70771
VERSION ARI70771.1 GI:17908730
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1166)
AUTHORS Stout,J.T., Luu,H.T., Hanson,S.F., Maxwell,D.P., Ahlquist,P.G. and
Gilbertson,R.L.
TITLE Transgenic plants expressing mutant geminivirus AC1 or CI genes
JOURNAL Patent: US 6291743-A 13 18-SEP-2001;
FEATURES
source location/Qualifiers
1..1166
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Query Match 95.5%; Score 1033.8; DB 6; Length 1166;
Best Local Similarity 97.6%; Pred. No. 1e-288;
Matches 1061; Conservative 0; Mismatches 22; Indels 4; Gaps 1;
QY 1 ATGCCCCCAAGAAATTTAGAGTTCAAGTCAAGAACTATTCTTAATTCCTCCAG 60
Db 44 ATGCCCCCAAGAAATTTAGAGTTCAAGTCAAGAACTATTCTTAATTCCTCCAG 103
QY 61 TGTCTCTATCTAAAGAGAGCACTTCCCAATTCAAAACCTAAATACCCAGTCAAC 120
Db 104 TGTCTCTATCTAAAGAGAGCACTTCCCAATTCAAAACCTAAATACCCAGTCAAC 163
QY 121 AAGAAATTCATCAAAATTTGCAAGAGCTTCATGAATAATGGGAACTCATCTCCATGTG 180
Db 164 AAGAAATTCATCAAAATTTGCAAGAGCTTCATGAATAATGGGAACTCATCTCCATGTG 223
QY 181 CTGTGTCAGTTGAGAGTAAGTACCAATGACGAATCAAGATTTCTTCACTGCTGCTCC 240
Db 224 CTGTGTCAGTTGAGAGTAAGTACCAATGACGAATTTCTTCACTGCTGCTGCTCC 283
QY 241 CCNACCCGGTCAAGATTTCCATTCGATATTCAAGAGAGCTTAATCGAGCTCCAGCTC 300
Db 284 CCNACCCGGTCAAGATTTCCATTCGATATTCAAGAGAGCTTAATCGAGCTCCAGCTC 343
QY 301 AATCATACATGACAGAGCGAGATACCAATGGAATGGGAGATTTCAGAAATCGACGCG 360
Db 344 AATCATACATGACAGAGCGAGATACCAATGGAATGGGAGATTTCAGAAATCGACGCG 403
QY 361 A----GATCTGCCAGAGAGCGCAGACGTCGTCTAATGATTCAATATGCGAAAGCATTA 416

Db 404 AGATCATCTGCCAGAGAGCGCAGACGTCGTCTAATGATTCAATATGCGAAAGCGTTAA 463
QY 417 TCGAGGTGCGTTCAATCTGCTTAGCGGTCTTAAGGGAAGAAACAACAAAGATTGTTGT 476
Db 464 TCGAGGTGCGTTCAATCTGCTTAGCGGTCTTAAGGGAAGAAACAACAAAGATTGTTGT 523
QY 477 ATTCAAAATCATTAATCTGCTTAGCGGTCTTAAGGGAAGAAACAACAAAGATTGTTGT 536
Db 524 ATTCAAAATCATTAATCTGCTTAGCGGTCTTAAGGGAAGAAACAACAAAGATTGTTGT 583
QY 537 GTGGGTCTCTCAATTTCAAGTCTCTTCTTCACTAAGTCTCTCAAGAGATGAGAGAAAG 596
Db 584 GTGGGTCTCTCAATTTCAAGTCTCTTCTTCACTAAGTCTCTCAAGAGATGAGAGAAAG 643
QY 597 GCGGATTAATTAATTTGCGAGCGGTGACGCTCGCGCGGATAGACTGTAAGTATCAT 656
Db 644 GCGGATTAATTAATTTGCGAGCGGTGACGCTCGCGCGGATAGACTGTAAGTATCAT 703
QY 657 CGTGAAGGTGATTCAGAAACAGGAAACAGATGTGGGCGCGTTCAGGCCACATTA 716
Db 704 CGTGAAGGTGATTCAGAAACAGGAAACAGATGTGGGCGCGTTCAGGCCACATTA 763
QY 717 CTATCTCAGTGAACCTAGACTTCAATGCTGAGTCTTCTGAAATGATGACATTA 776
Db 764 CTATCTCAGTGAACCTAGACTTCAATGCTGAGTCTTCTGAAATGATGACATTA 823
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Db 824 CGTATTTGATGACATGACCGCATTTATTAAGCTAAAGCACTGGAAGAAATTTGCTGAG 883
QY 837 GCGCCAGAAAGATTGGCAATCAAAATTGCAAGTACGTAACCGATTCATTAAGCGCG 896
Db 884 GCGCCAGAAAGATTGGCAATCAAAATTGCAAGTACGTAACCGATTCATTAAGCGCG 943
QY 897 AATCCAGCAATCTGCTTTCGAATCTGCTGAGTACGCTGACCTTAAGAGTTCTTA 956
Db 944 AATCCAGCAATCTGCTTTCGAATCTGCTGAGTACGCTGACCTTAAGAGTTCTTA 1003
QY 957 CAAGAGAAATTAACGATCTCAAGAACTGACATCAAGAAATGCGATCTTCAACCGCT 1016
Db 1004 CAAGAGAAATTAACGATCTCAAGAACTGACATCAAGAAATGCGATCTTCAACCGCT 1063
QY 1017 CACAGCCCCCTCTATCAAGAGAGACACAGCGCAAGCAAGAAACGGCAATCAGAGCG 1076
Db 1064 CACAGCCCCCTCTATCAAGAGAGACACAGCGCAAGCAAGAAACGGCAATCAGAGCG 1123
QY 1077 GCAGGCT 1083
Db 1124 GCAGGCT 1130

RESULT 9
AF049336/c 2642 bp DNA linear VRL 06-MAR-1998
LOCUS AF049336
DEFINITION Sida golden mosaic virus coat protein (AV1), AC3 (AC3),
transactivator protein (AC2), replication associated protein (AC1),
and AC4 (AC4) genes, complete cds.
ACCESSION AF049336
VERSION AF049336.1 GI:2935539
KEYWORDS Sida golden mosaic virus
SOURCE Sida golden mosaic virus
ORGANISM Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE 1 (bases 1 to 2642)
AUTHORS Abouzid,A.M., Polston,J.E. and Hiebert,E.
TITLE Molecular characterization of a geminivirus infecting Sida
santaremensis in Florida
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2642)
AUTHORS Abouzid,A.M., Polston,J.E. and Hiebert,E.
TITLE Direct Submission
JOURNAL Submitted (19-FEB-1998) Plant Pathology, University of Florida,

1435 Fifield Hall, PO Box 110680, Gainesville, FL 32611-0680, USA
location/Qualifiers

FEATURES

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rep_origin

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ORIGIN

Query Match

83.6%; Score 905.6; DB 14; Length 2642;

Best Local Similarity 89.9%; Pred. No.1,9e-251;
Matches 971; Conservative 0; Mismatches 109; Indels 0; Gaps 0;

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Db	2102	GTTCTCTCATTTCAAGTCTTCTTTCACTAAGTTCCTGACGAGATGACGAATGGGCG	2043
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Qy	781	ATTGATGACATCCGACCGCATTTCTTAAAGCTTAAAGCATGGAAGAAATGCTGGGGCC	840
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Qy	841	CAGAAAGATTGGCAATCAAAATTCGAATGCGTAAAGCAGTCAATTAAGCGCGAATC	900
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Qy	901	CCAGCAATCGTCTTTGCAATCTCTGTCAGAGGTGCCAGCTATAAAGGTTCTTAGACAAA	960
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Qy	961	GCAAAATATCAGAGTCTCAAGAACTGACATCAAGATACGATCTTCATCACCTTCACA	1020
Db	1682	GAGAAATATCAGAGTCTCAAGAACTGACATCAAGATACGATCTTCATCACCTTCACA	1623
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Db 1622 GCCCCCTCTATCAGCAACACACAGCGCCAGGAGGCGCATACGAGGCGGAG 1563

RESULT 10
LOCUS GEABVVA/2632 bp DNA circular VRL 21-NOV-2003
DEFINITION Abutillon mosaic virus subgenome DNA A.
ACCESSION X15983
VERSION X15983.2 GI:38490457
KEYWORDS circular; coat protein; structural protein.
SOURCE Abutillon mosaic virus
ORGANISM Abutillon mosaic virus
virus; sedna viruses; Geminiviridae; Begomovirus.

REFERENCE 1 (bases 1 to 2632)
AUTHORS Frieschmidt, T., Zimmert, G. and Jeske, H.
TITLE The nucleotide sequence of abutillon mosaic virus reveals
virology 178 (2), 461-468 (1990)

JOURNAL MEDLINE 91020984
PUBMED 2219703
REFERENCE 2 (bases 1 to 2632)
AUTHORS Jeske, H.
TITLE Direct Submission
JOURNAL Submitted (26-JUL-1989) Jeske H., Institut f. Allgemeine Botanik,
Universitaet Hamburg, Ohnhorst str 18, 2000 Hamburg 52, F R G
REMARK revised by [3]

REFERENCE 3
AUTHORS Jeske, H.
TITLE Direct Submission
JOURNAL Submitted (29-NOV-1990)
REMARK revised by [4]
AUTHORS Jeske, H.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2003) Jeske H., Biologisches Institut,
Pfefferwaldring 57, D-70550 Stuttgart, GERMANY
COMMENT On Nov 21, 2003 this sequence version replaced gi:59349.
FEATURES
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ORIGIN
Query Match 79.1%; Score 856.4; DB 14; Length 2632;
Best Local Similarity 87.3%; Pred. No. 3,7e-237;
Matches 938; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

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2572 ACTAAGAGAGCACTTCCCAATTAAGAACTTAATACCCAGTCAAGAAATTC 2513
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2512 ATCAAAATTTGAGAGCTTCAAGTCAAGAACTTAATACCCAGTCAAGAAATTC 2453
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OY	490	AACATTCGCTCTAATCTGAAGAAAGATTTGCCAAAAGGCTCCGGAACCGTGGGTTCCTCCA	549
Db	2152	AACATTCGCTCTAATCTGAAGAAATATTCGAAAAGGCTCCGGAACCATGAGTTTCGGGG	2093
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OY	670	TCAAGAACAGGGAAGACGATGTGGCGCGTGCCTTAGGCGCCACATTAATATCTCAGTGA	729
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OY	850	TGCGCATCAAAATTGCAAGTACGTTAAGCCGATTCGTAATTTAAAGCGGAAATCCAGCAATC	909
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OY	910	GTGCTTTGCAATCCGTGTGAGGGGTGCAGGCTATTAAGAGTCTTATGACAAAGCAGAAAT	969
Db	1732	GTGCTTTGCAATCCGTGTGAGGGGTTCAGGCTATTAAGAGTACCTGGAACAAAGAGAAAT	1673
OY	970	ACAGGCTCAAGAACTGGACTATCAAGATCGATCTTCATCACCTTCAGACCCCTCTC	1029
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Db	1612	TATCAAGAGACACACAGGCAAGCCAAAGAGAGGCAATTAAGCGGCGCGAGAGAT	1559

RESULT 11	AMU51137/c	2634 bp	DNA	circular VRL 07-MAR-2003
LOCUS	AMU51137/c			
DEFINITION	Abutilon mosaic virus-HW AV1, AC3, AC2, AC1, and AC4 genes,			
ACCESSION	AMU51137			
VERSION	U51137			
KEYWORDS	complete cds.			
SOURCE	U51137.1 GI:1657740			
ORGANISM	Abutilon mosaic virus-HW			
REFERENCE	Abutilon mosaic virus-HW			
AUTHORS	Vinases; ssDNA viruses; Geminiviridae; Begomovirus.			
TITLE	1 (bases 1 to 2634)			
JOURNAL	Wu,Z.C.Hu,J.S.Polston J.E., Ullman,D.E. and Hiebert,E.			
REFERENCE	Complete nucleotide sequence of a non-vector transmissible strain			
AUTHORS	of abutilon mosaic geminivirus			
TITLE	Phytopathology 86 (6), 608-613 (1996)			
JOURNAL	2 (bases 1 to 2634)			
REFERENCE	Wu,Z.C.Hu,J.S.Polston J.E., Ullman,D.E. and Hiebert,E.			
AUTHORS	Direct Submision			
TITLE	Submitted (12-MAR-1996) Plant Pathology, University of Hawaii, 3190			
JOURNAL	Malie Way, Honolulu, HI 96822, USA			
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ORIGIN					
Query Match	77.6%;	Score 840.4;	DB 14;	Length 2634;	
Best Local Similarity	86.4%;	Pred. No. 1.6e-232;			
Matches 928;	Conservative 0;	Mismatches 146;	Indels 0;	Gaps 0;	
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QY 70 TCTAAGAGAGACATTTCCCAATTACAAAACCTAAATACCCAGTCAACAGAAATTC 129
DB 2574 GCCAAAGAGGTGGACATTTCCCAATTACAAAACCTAGAAAACCGGTAACAGAAATTC 2515
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QY 250 TCAGACATTTCCATCCGAATTAATCAGGAGCTTAATGAGCTCCAGCTCAATCATAC 309
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QY 310 ATGACAGAGAGCGAGATACCAATGAGGAGATTTCCAAATTCAGCGGAGATCTGCC 369
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DB 2154 AACATCGGCTCTAACCTAAGAAAGATTTGCGAAAGGCTCCGGAACCGTGGTTCCTCCG 2095
QY 550 TTTCAAGTCTCTTTCACTAAAGTCTGACAGAGATGAGGAGATGGGAGATTAAT 609
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RESULT 12
AF101476/c
LOCUS AF101476 2634 bp DNA circular VRL 07-MAR-2003

DEFINITION Chino del tomate virus-[IC] component A, AV1 protein, AC3 protein, AC2 protein, AC1 protein, and AC4 protein genes, complete cds.
ACCESSION AF101476
VERSION AF101476.1 GI:4336693
KEYWORDS Chino del tomate virus-[IC]
SOURCE Chino del tomate virus-[IC]
ORGANISM Viruses; sedna viruses; Geminiviridae; Begomovirus.
REFERENCE 1 (bases 1 to 2634)
AUTHORS Jiang, H., Hou, Y.-M., Guzman, P. and Gilbertson, R.L.
TITLE Complete nucleotide sequence of the infectious clone of tomato leaf crumple geminivirus
JOURNAL (in) ANNUAL MEETING OF THE AMERICAN PHYTOPATHOLOGICAL SOCIETY, PHYTOPATHOLOGY, VOL 88 (SUPPL): S44;
(1998)
2 (bases 1 to 2634)
AUTHORS Jiang, H., Hou, Y.-M., Guzman, P. and Gilbertson, R.L.
TITLE Direct Submission
JOURNAL Submitted (26-OCT-1998) Plant Pathology, University of California, Davis, One Shields Ave., Davis, CA 95616, USA
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181 CTGTTCAGTTGAAAGGTAAAGTACCAATGCAAGAAACAGATTTCTTGCAGCTGTCTCC 240
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 ACCESSION
 AJ563919
 VERSION
 AJ563919.1 GI:31044057
 KEYWORDS
 AC1 gene; AV1 gene; coat protein; replicase.
 SOURCE
 Tomato mottle Taino virus
 ORGANISM
 Viruses; ssDNA viruses; Geminiviridae; Begomovirus.

REFERENCE
 1
 Hernandez, L.
 Caracterizacion molecular de geminivirus en papa (Solanum tuberosum L.)
 Tesis (2000) Department of Biology, Universidad de La Habana, Ciudad de La Habana, Cuba

REFERENCE
 2
 Cordero, M., Ramos, P. L., Hernandez, L., Fernandez, A. I., Echemendia, A. L., Peral, R., Gonzalez, G., Garcia, D., Valdes, S., Beleviez, A. and Hernandez, K.
 Identification of Tomato mottle Taino begomovirus strains in Cuban potato fields
 Unpublished
 3 (bases 1 to 2155)
 Ramos, P. L.
 Direct Submission
 Submitted (20-MAY-2003) Ramos P. L., Plantas, Centro Ingenieria Genetica y Biotecnol., Ave 31 e/ 158 y 190 Cubanacan, Playa, Ciudad de La Habana, 10600, CUBA

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ORIGIN

ATVKNDLRDRYOMRPHTKVTCGOYASNEOLVRRPFWKNNHVVYNNHOEAAKYENHT
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Best Local Similarity 85.9%; Pred. No. 4.8e-228;
Matches 915; Conservative 0; Mismatches 150; Indels 0; Gaps 0;

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RESULT 14
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LOCUS
DEFINITION
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ACCESSION
AF012300
VERSION
AF012300.1 GI:2317786
KEYWORDS
SOURCE
Tomato mottle Taينو virus
ORGANISM
Tomato mottle Taينو virus
REFERENCE
1 (bases 1 to 2597)
Ramos, P.L., Guerra, O., Peral, P., Oramas, P., Guevara, R.G. and
Rivers, B.D. 1997. A new bipartite geminivirus from Cuba
Rivers, B.D. 1997. In press
2 (bases 1 to 2597)
Ramos, P.L., Oramas, P., Guevara, R.G. and Rivers, B.D. 1997. A new bipartite geminivirus from Cuba
Rivers, B.D. 1997. In press
Submitted (02-JUL-1997) Ingenieria Genetica, CINVESTAV Irapuato,
Apo Postal 629, Irapuato, Gto 36500, Mexico
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ORIGIN

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Best Local Similarity 85.7%; Pred. No. 4,2e-227;
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LOCUS
DEFINITION
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replication enhancement protein (AC3), transcriptional activator
protein (AC2), replication initiator protein (AC1), and AC4 gene,
complete cds.
ACCESSION
AF226664
GI:7109259
VERSION
AF226664.1
KEYWORDS
Chino del tomate virus-[H8]
ORGANISM
Chino del tomate virus-[H8]
VIRUSES; ssDNA viruses; Geminiviridae; Begomovirus.
REFERENCE
1 (bases 1 to 2635)
Brown,J.K. and Nelson,M.R.
Transmission, host range, and virus-vector relationships of chino
del tomate virus, a whitefly-transmitted geminivirus from Sinaloa,
Mexico
Plant Dis. 72, 866-869 (1988)
2 (bases 1 to 2635)
Brown,J.K., Ostrrow,K.M., Idris,A.M. and Stenger,D.C.
Chino del tomate virus: relationships to other begomoviruses and
the identification of A component variants that affect symptom
expression
Phytopathology 90, 546-552 (2000)
3 (bases 1 to 2635)
Stenger,D.C. and Brown,J.K.
Direct Submission
Submitted (20-JAN-2000) USDA-ARS, University of Nebraska at
Lincoln, 344 Keim Hall, Lincoln, NE 68583, USA
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Best Local Similarity 84.7%; Pred. No. 7.9e-226;
Matches 917; Conservative 0; Mismatches 166; Indels 0; Gaps 0;
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QY 61 TGGCTCTTCTAAGAGAGCACTTCCCAATTACAAAACCTAATAATCCCGAGTCAAC 120
Db 2442 TGGCTCTTCTAAGAGAGCACTTCCCAATTACAAAACCTAATAATCCCGAGTCAAC 2383
QY 121 AAGAAATTCATCAAAATTGCGAGAGCTTCATGAAATGGGAACCTCATCTCCATGTG 180
Db 2382 AAGAAATTCATCAAGATCTGCGAGAGTTCATGAGAAATGGGAACCGCATCTCCAGT 2323
QY 181 CTGTTCAGTTCAAGAGTAAAGTCAATGCAAGATTAAGATTTCTGACCTGCTCC 240
Db 2322 CTGATCAATTCGAAGAGTACAGTCAAGATTAAGATTTCTGATCTGCTCC 2263
QY 241 CCAATCCGCTGACGACATTTCCATCCGAATATTCAGGAGCTTAATCGAGCTCCAGTCC 300
Db 2262 CCAATCCGCTGACGACATTTCCATCCGAATATTCAGGAGCTTAATCGAGCTCCAGTCC 2203
QY 301 AATCATATCATGCAAGAGAGATACATGAATGGGAGATTTCCAAATCGACGCC 360

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Db 2202 AAGTCTCAATGACACAGAGCGAGATPACAGTTGAGTGGGAGAAATTCAGATCGACGCC 2143
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QY 601 GATPAAATTTTGGGACGCGGTGACGCTGCGCGCGGATPAGACTGTAAATCATCTG 660
Db 1902 GATPAAATTTTGAAGAGAGTTCCTGCGCGCGGAGAGACTTAATGATCATCTG 1843
QY 661 GAGGCTGATTCAGAGAGAGAGAGATGTCGCGCGCGGATPAGACTGTAAATCATCTAT 720
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QY 1081 GGT 1083
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Gapop 10-0 , Gapext 1.0

Searched: 413486 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1047.8	96.7	1160	2	AAT93294 Tomato mo
2	1044.6	96.5	1169	2	AAT93283 Tomato mo
3	1043	96.3	1169	2	AAT93284 Tomato mo
4	1040.8	96.1	1169	2	AAT93309 Tomato mo
5	1038.2	95.9	1169	2	AAT93282 Tomato mo
6	1033.8	95.5	1169	2	AAT93285 Tomato mo
7	702.2	64.8	1246	2	AAT93286 Tomato mo
8	696.2	64.3	1183	2	AAT93314 Bean gold
9	696.2	64.3	1651	3	AA94700 Bean gold
10	696.2	64.3	1894	3	AA94703 Bean gold
11	696.2	64.3	2072	3	AA94702 Bean gold
12	694.6	64.1	1183	2	AAT93290 Bean gold
13	694.6	64.1	1651	3	AA94701 Bean gold
14	691.2	63.8	1062	2	AAT93291 Bean gold
15	691.2	63.8	1062	2	AAT93292 Bean gold
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20	494.4	45.7	1080	2	AA94630 Tomato ye
21	492.8	45.5	1080	2	AA94630 Tomato ye

22	492.8	45.5	1080	2	AAT12904 Sardinian
23	479.4	44.3	1145	2	AAT93287 Tomato ye
24	479.4	44.3	1145	2	AAT93288 Tomato ye
25	479.4	44.3	1145	2	AAT93311 Tomato ye
26	476.2	44.0	1145	2	AAT93289 Tomato ye
27	474	43.8	2739	2	AAT93289 Tomato ye
28	448	41.4	2766	2	AA929761 Tobacco l
29	421.2	38.9	2723	1	AA970893
30	419.6	38.7	1083	1	AA970897 ORF 4 firo
31	418.4	38.6	2744	2	AAT93317 Tomato le
32	304.4	28.1	691	8	ABV76265 Tomato ye
33	259.4	24.0	506	8	ABV76265 Tomato ye
34	259.4	24.0	506	8	ABV76265 Tomato ye
35	259.4	24.0	508	8	ABV76264 Tomato ye
36	251	23.2	550	2	AA94375 Tomato le
37	246.6	22.8	1403	2	AAT93318 Tomato-in
38	243.8	22.5	550	2	AA94377 Tomato le
39	238.2	22.0	550	2	AA94376 Tomato le
40	185.2	17.1	780	2	AAT93319 Tomato-in
41	183.8	17.0	479	2	AA94372 Gemini vi
42	162	15.0	297	1	AA970900 ORF 7 firo
43	158	14.6	434	2	AA94371 Gemini vi
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45	50.2	4.6	795	3	AA949876 Wheat dwa

ALIGNMENTS

RESULT 1	AA93294	standard; DNA; 1160 BP.
ID	AA93294	standard; DNA; 1160 BP.
AC	AA93294	
XX	17-OCT-2003 (revised)	
DT	27-APR-1998	(first entry)
XX	Tomato mottle virus AC1 open reading frame.	
XX	Geminivirus; TOMOV; AC1 gene; transdominant mutation; transgenic plant;	
XX	disease resistance; ss; cyclic; circular.	
XX	Tomato mottle virus; isolate Florida.	
OS	Tomato mottle virus; isolate Florida.	
XX	Key	Location/Qualifiers
XX	CDS	44..1129
XX	FT	/*tag= a
XX	FN	W09739110-AL.
XX	PD	23-OCT-1997.
XX	PF	15-APR-1997; 97MO-US006300.
XX	PR	16-APR-1996; 96US-001517P.
XX	PA	(SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX	PA	(WISC) WISCONSIN ALUMNI RES FOUND.
XX	PI	Scout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
XX	XX	WPI; 1997-526447/48.
XX	XX	P-PSDB; AA94332.
XX	XX	Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
XX	XX	genes - have increased resistance to geminivirus infection e.g. tomato
XX	XX	mottle virus, tomato yellow leaf curl virus or bean golden mosaic
XX	XX	geminivirus.
XX	XX	Example 3.3; Page 57-58; 132bp; English.
XX	XX	This genomic DNA sequence includes the open reading frame of the wild-

CC type AC1 gene of tomato mottle virus (ToMoV), a geminivirus that has a
CC bipartite genome. The AC1 gene must be expressed for efficient
CC replication of the two genomic components, DNA-A and DNA-B. It encodes a
CC protein (see AAW34325) having a DNA binding site specific to the DNA-A
CC common region, a DNA nicking activity, and an NTP binding activity. The
CC invention involves production of transgenic plants containing DNA
CC comprising AC1 or CI wild-type or mutant sequences that negatively
CC interfere in trans with geminiviral replication during infection. Such
CC transgenic plants are resistant to viral infection. The AC1/CI genes are
CC especially from ToMoV, tomato yellow leaf curl virus or bean golden
CC mosaic geminivirus (see AAT93282-93) and encode polypeptides (see
CC AAW34324-35) that have mutations in the highly conserved DNA-nicking
CC domain and/or the NTP-binding domain. (Updated on 17-OCT-2003 to
CC standardise OS field)
XX

SQ Sequence 1160 BP; 360 A; 276 C; 257 G; 267 T; 0 U; 0 Other;
Query Match 96.7%; Score 1047.8; DB 2; Length 1160;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1061; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTCACTTATCCCAAG 60
DB 44 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTCACTTATCCCAAG 103
QY 61 TGGCTCTATCTAAGAAAGACCTTCCCAATTACAAACCTAAATACCCCAAGTCAAC 120
DB 104 TGGCTCTATCTAAGAAAGACCTTCCCAATTACAAACCTAAATACCCCAAGTCAAT 163
QY 121 AAGAAATTCATCAAAATTTTGAGAGAGCTTCATGAAATGGGGAACCTCATCTTCATGTG 180
DB 164 AAGAAATTCATCAAAATTTTGAGAGAGCTTCATGAAATGGGGAACCTCATCTTCATGTG 223
QY 181 CTGTGTTAGTTCCAGAGTAAATGATCAATGCAAGATTAACAGATTCTTCGACTGCTCC 240
DB 224 CTGTGTTAGTTCCAGAGTAAATGATCAATGCAAGATTAACAGATTCTTCGACTGCTCC 283
QY 241 CCAACCCGGTCAGACATTTTCATCGAATATTGAGGAGCTAAATGAGAGTCCGAGTCC 300
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QY 301 AAATCATACATCGAAGAGAGAGATTAATCGAATGGGAGATTTCGAATGACGGC 360
DB 344 AAATCATACATCGAAGAGAGAGATTAATCGAATGGGAGATTTCGAATGACGGC 403
QY 361 AGATCTGCCAGAGAGAGAGAGAGATTAATCGAATGGGAGATTTCGAATGACGGC 420
DB 404 AGATCTGCCAGAGAGAGAGAGAGATTAATCGAATGGGAGATTTCGAATGACGGC 463
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DB 464 AGTTCGGTTCAATCTGCTTACGCTTCTAAGGGAAGAACCAAGATTTTGTATTA 523
QY 481 CAAATCATACATCGCTCTTACCTTAAAGAAATTTGCGAAAGGCTCCGGAACCGTGG 540
DB 524 CAAATCATACATCGCTCTTACCTTAAAGAAATTTGCGAAAGGCTCCGGAACCGTGG 583
QY 541 GTTCTCTCATTTCAAGTCTCTTTCTTCACTTAAGTTCTTCAAGAGATGCGAATGGGCG 600
DB 584 GTTCTCTCATTTCAAGTCTCTTTCTTCACTTAAGTTCTTCAAGAGATGCGAATGGGCG 643
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DB 644 GATATATTTTGGGAGCGGTGACGCTGCGCCGCGATAGACCTGTAAGTATCATGCTC 703
QY 661 GAGGGTATTTCAAGAACGAGGAGACGATGTGGCGGTGGTGGTGGCCCAATTAAT 720
DB 704 GAGGGTATTTCAAGAACGAGGAGACGATGTGGCGGTGGTGGTGGCCCAATTAAT 763
QY 721 CTGAGTGAACCTTAAGCTTCAATGCTGAGTCTTTCTGCAATGATGTCAGTATTAAGCTC 780
DB 764 CTGAGTGAACCTTAAGCTTCAATGCTGAGTCTTTCTGCAATGATGTCAGTATTAAGCTC 823

QY 781 ATTGATGACATCGACCGCATTTATCTTAAGCTAAAGCATGGAAGATTTGCTGGGGCC 840
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QY 841 CAGAAAGATTGGCAATCAATTAATGCAAGTACGTAAGCCAGTTCAATTAAGGCGGAATC 900
DB 884 CAGAAAGATTGGCAATCAATTAATGCAAGTACGTAAGCCAGTTCAATTAAGGCGGAATC 943
QY 901 CCGAATCTGCTTTGCAATCTCTGTGAGAGGTCGCGCATTAAGAGTTCTTAAGACAA 960
DB 944 CCGAATCTGCTTTGCAATCTCTGTGAGAGGTCGCGCATTAAGAGTTCTTAAGACAA 1003
QY 961 CGAATAATCAGGTCCTCAAGACTGAGTATCAAGATCGATCTTCATCACCTCACA 1020
DB 1004 CGAATAATCAGGTCCTCAAGACTGAGTATCAAGATCGATCTTCATCACCTCACA 1063
QY 1021 GCCCCCTCTATCAAGAGACACACAGGCAAGCCAAAGACGCGCAATCGAAGCGCAG 1080
DB 1064 GCCCCCTCTATCAAGAGACACACAGGCAAGCCAAAGACGCGCAATCGAAGCGCAG 1123
QY 1081 GGT 1083
DB 1124 GGT 1126

RESULT 2

AAT93283
ID AAT93283 standard; DNA; 1169 BP.

XX AAT93283;

DT 27-APR-1998 (first entry)

DE Tomato mottle virus AC1 mutant ToMoV-AC1d1m1 gene.

XX Geminivirus; ToMoV-AC1d1m1; AC1 gene; transdominant mutation;

KM transgenic plant; disease resistance; ss; cyclic; circular.

XX Tomato mottle virus; isolate Florida.

OS Synthetic.

XX Key Location/Qualifiers

FT CDS 44..1129

FT CDS /*tag= a

XX W09739110-A1.

XX 23-OCT-1997.

PD 15-APR-1997; 97MO-US006300.

XX 16-APR-1996; 96US-0015517P.

PR (SEMI-) SEMINIS VEGETABLE SEEDS INC.

PA (WISC) WISCONSIN ALUMNI RES FOUND.

PI Scout UT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;

XX WPI, 1997-526447/48.

DR P-PSDB; AAW34325.

PT Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant

PT genes - have increased resistance to geminivirus infection e.g. tomato

PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic

PT geminivirus.

PS Claim 11; Page 64-65; 132pp; English.

XX This DNA sequence comprises a transdominant lethal mutant, designated

CC ToMoV-AC1d1m1, of the AC1 gene of tomato mottle virus (ToMoV). It

CC encodes an AC1 protein (see AAW34325) that carries a mutation in its NTP-

CC binding domain. The AC1 gene (see also AAT93294) must be expressed for

CC efficient replication of the two genomic components, DNA-A and DNA-B, of

the bipartite Tomato genome. The invention involves production of transgenic plants containing DNA comprising geminivirus AC1 or CI wild-type or mutant sequences that negatively interfere in trans with geminiviral replication during infection. Such transgenic plants are resistant to viral infection. The AC1/CI genes are especially from Tomato, tomato yellow leaf curl virus or bean golden mosaic geminivirus (see AY93282-93) and encode polypeptides (see AA03324-35) that have mutations in the highly conserved DNA-nicking and/or the NTP-binding domains

SQ Sequence 1169 BP; 361 A; 280 C; 258 G; 270 T; 0 U; 0 Other;

Query Match	Score	DB 2;	Length
96.5%	1044.6;		1169;

Matches 1059; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY	1	ATGCCCCACCAAGAAATTTAGATTGACGTCAAGAACTATTTCTTAATTATCCCG	60
Db	44	ATGCCCCACCAAGAAATTTAGATTGACGTCAAGAACTATTTCTTAATTATCCACAG	103
QY	61	TGCTCTCTATTTAAGAAAGCACTTTTCCCAATTACAAACCTTAATTCGCCAGTCAAC	120
Db	104	TGCTCTTGTCTTAAAGAAAGCACTTTTCCCAATTACAAACCTTAATTCGCCAGTCAAT	163
QY	121	AAGAAATTCATCAAAATTTGCGAGAGGCTCATGAAATTTGGGGAACCTCATCCATGNG	180
Db	164	AAGAAATTCATCAAAATTTGCGAGAGGCTCATGAAATTTGGGGAACCTCATCTCCATGTG	223
QY	181	CTTGTTCAGTTCGAAGGTAAAGTACCAATGACGAATTAACAGATTTTCGACCTGTCTCC	240
Db	224	CTTGTTCAGTTCGAAGGAAGTAAACAGTGCAGATTAACAGATTTTCGACCTGTGCTCC	283
QY	241	CCAAACCCGGTCAGACATTTTCATCCCGAAATTTACAGGAGCTTAATTCAGCTCCGACGC	300
Db	284	CCAAACCCGGTCAGACATTTTCATCCCGAAATTTACAGGAGCTTAATTCAGCTCCGACGC	343
QY	301	AAATCATACATCGACAAGAGACGAGATCAATCGATGGGAGATTTCCAAATCGACGCG	360
Db	344	AAATCGTACATCGACAAGAGACGAGATCAATCGATGGGAGATTTCCAGATCGACGCG	403
QY	361	AGATCTGCCAGAGAGGCGCAGAGTCTGTCTAATGATTCAATTCGAAAGCATTTAAATGCA	420
Db	404	AGATCTGCCAGAGAGGCGCAGAGTCTGTCTAATGATTCAATTCGAAAGCGTTAAATGCA	463
QY	421	GGTTCGGTCAATCTGCCTTAGCGGTTCTAAGGGAAGAACCAACCAAGATTTTGAATTA	480
Db	464	AGTTCGGTCAATCTGCCTTAGCGGTTCTAAGGGAAGAACCAACCAAGATTTTGAATTA	523
QY	481	CAAAATCATTAACATCCGCTCTTAACCTAGAACGAATATTCGCAAAAGGCTCCGAAACCGTGG	540
Db	524	CAAAATCATTAACATCCGCTCTTAACCTAGAACGAATATTCGCAAAAGGCTCCGAAACCGTGG	583
QY	541	GTTTCTCTCATTTCAAGTCTCTTTCTTTCACTAACGTTTCTGACAGAGATGCAAGATGGGCG	600
Db	584	GTTTCTCTCATTTCAAGTCTCTTTCTTTCACTAACGTTTCTGACAGAGATGCAAGATGGGCG	643
QY	601	GATTAATTAATTTCCGGAGACGGGTGACGCTGCGCGCGCGGATAGACCTGTAAAGTATCAATCGTC	660
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QY	661	GAGGGTGAATTCAGAACAGGGAAGACGATGTGGGCGCGTGCCTTAGGCCCATTAACCTAT	720
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QY	721	CTCAGTGGACCTTAGAATTTCAATGGTGAAGTCTTCTGAAATGATGTGCAATTAACGTC	780
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QY	1081 GGT 1083	
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RESULT 3
AAT93284
ID AAT93284 standard; DNA; 1169 BP.

AC AAT93284 ;

DT 27-APR-1998 (first entry)

DE Tomato mottle virus AC1 mutant TOMOV-AC1d1m23 gene.

KW GeminiVirus; ToMoV-Ac1dIm23; AC1 gene; transdominant mutation
transgenic plant; disease resistance; ss; cyclic; circular.

OS	Tomato mottle virus; isolate Florida.
OS	Synthetic.

FH Key

ET

PN WO9739110

PD 23-OCT-19

PF 15-APR-19

PR 16-APR-19

PA (SEMI-) S

XX

XX XX

DR P-PSDB; A

PT Transgenic

PT mottle v.

21

[illegible]

CC TOMOV-ACI

CC binding c

CC the bipar

type or π

CC resistant

CC tomato yellow leaf curl virus or bean golden mosaic geminivirus (see
 CC AAT93382-93) and encode polypeptides (see AAM3324-35) that have
 CC mutations in the highly conserved DNA-nicking and/or the NTP-binding
 CC domains
 CC XX

Sequence 1169 BP; 364 A; 278 C; 257 G; 270 T; 0 U; 0 Other;

Query Match 96.3%; Score 1043; DB 2; Length 1169;
 Best Local Similarity 97.7%; Pred. No. 0;
 Matches 1058; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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QY 1 ATGCCCCCACCAGAAATTTAGAGTTCAAGTCAAGAACTATTTCTTAATCTATCCCG 60
DB 44 ATGCCCCCACCAGAAATTTAGAGTTCAAGTCAAGAACTATTTCTTAATCTATCCAG 103
QY 61 TGCCTCTATTAAGAAAGACACTTCCCAATTTACAAAACCTTAATCCCGCTCAAC 120
DB 104 TGCCTCTATTAAGAAAGACACTTCCCAATTTACAAAACCTTAATCCCGCTCAAT 163
QY 121 AAGAAATTCATCAAAATTTGAGAGAGCTCATGAAAAAGGGAACCTCATCTCATGTG 180
DB 164 AAGAAATTCATCAAAATTTGAGAGAGCTCATGAAAAAGGGAACCTCATCTCATGTG 223
QY 181 CTGTGTCAGTTCGAAAGTAACTACCAATGACAGATTAACAGATTCTTGACCTGTCTCC 240
DB 224 CTGTGTCAGTTCGAAAGTAACTACCAATGACAGATTAACAGATTCTTGACCTGTCTCC 283
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QY 481 CAAATATCATCATCGGCTCTTAACCTAGAGAGATTTGCGAAAGCTCCGGAACCGTGG 540
DB 524 CAAATATCATCATCGGCTCTTAACCTAGAGAGATTTGCGAAAGCTCCGGAACCGTGG 583
QY 541 GTTCCCTCAATTCAGTCTCTTTCTTTCACTAACGTTCTCTGACGAGATGCAAGAAATGGCGG 600
DB 584 GTTCCCTCAATTCAGTCTCTTTCTTTCACTAACGTTCTCTGACGAGATGCAAGAAATGGCGG 643
QY 601 GATAATTAATTTCCGGAGGGGTGACGCTCCGCCGCCGATACCTCTGTAAGTATCATGCTC 660
DB 644 GATAATTAATTTCCGGAGGGGTGACGCTCCGCCGCCGATACCTCTGTAAGTATCATGCTC 703
QY 661 GAGGGTATTCAGAAACAGGAGAGAGATGTGGCGCTGGTGGTGGCCCATATACAT 720
DB 704 GAGGGTATTCAGAAACAGGAGAGAGATGTGGCGCTGGTGGTGGCCCATATACAT 763
QY 721 CTCAGTGAACCTTAGACTTCATGTGTGAGTCTTTCTTGAAATGTGACATATACGTC 780
DB 764 CTCAGTGAACCTTAGACTTCATGTGTGAGTCTTTCTTGAAATGTGACATATACGTC 823
QY 781 ATTGATGACATCGGACCGCATTAATCTAAAGCTAAAGCACTGGAAGAAATGCTGGGGCC 840
DB 824 ATTGATGACATCGGACCGCATTAATCTAAAGCTAAAGCACTGGAAGAAATGCTGGGGCC 883
QY 841 CAGAAAGATTGGCAATCAAAATTTGCAAGTACGTAAGCAAGTTCATTAATTAAGCGGATC 900
DB 884 CAGAAAGATTGGCAATCAAAATTTGCAAGTACGTAAGCAAGTTCATTAATTAAGCGGATC 943
QY 901 CACGAATCGTGTCTTTGCAATCTGTGTGAGGGTCCAGCTTAAGAGTTCTTAAGACAA 960
  
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DB 944 CACGAATCGTGTCTTTGCAATCTGTGTGAGGGTCCAGCTATAAAGATTCTTAGACAA 1003
QY 961 GCAGAAATATACAGGTCTCAAGAACTGAGACTATCAAGATGAGATCTTCAATCACCCTACA 1020
DB 1004 GCAGAAATATACAGGTCTCAAGAACTGAGACTATCAAGATGAGATCTTCAATCACCCTACA 1063
QY 1021 GCCCCCTCTATCAAGAGACACACAGGACCCAGAAACCGGCAATCAGAAAGCCGAG 1080
DB 1064 GCCCCCTCTATCAAGAGACACACAGGACCCAGAAACCGGCAATCAGAAAGCCGAG 1123
QY 1081 GGT 1083
DB 1124 GGT 1126
  
```

RESULT 4
 AAT93309/c
 ID AAT93309 standard; DNA; 2602 BP.

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XX AAT93309;
AC 17-OCT-2003 (revised)
DT 27-APR-1998 (first entry)
DE Tomato mottle virus full-length A-component clone.
XX XX
XX Geminivirus; TOMOV; AC1 gene; transdominant mutation; transgenic plant;
XX XX
XX disease resistance; ser. cyclic; circular.
OS Tomato mottle virus; isolate Florida.
XX XX
XX W09739110-A1.
XX XX
XX 23-OCT-1997.
XX XX
XX 15-APR-1997; 97WO-US006300.
XX XX
XX 16-APR-1996; 96US-0015517P.
XX XX
XX (SEMT-) SEMINIS VEGETABLE SEEDS INC.
XX XX
XX (WISC) WISCONSIN ALUMNI RES FOUND.
XX XX
XX Stout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
XX XX
XX WPI; 1997-526447/48.
XX XX
XX Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
XX XX
XX genes - have increased resistance to geminivirus infection e.g. tomato
XX XX
XX mottle virus, tomato yellow leaf curl virus or bean golden mosaic
XX XX
XX geminivirus.
XX XX
XX Example 3.1; Page 76-77; 132pp; English.
XX XX
XX This genomic DNA sequence comprises a full-length A-component clone of
XX XX
XX tomato mottle virus (TOMOV), a geminivirus that has a bipartite genome
XX XX
XX comprising DNA-A and DNA-B. It was isolated from TOMOV infected Nicotiana
XX XX
XX benthamiana and tomato plant DNA by restriction digestion. The DNA-B
XX XX
XX component (see AAT93310) was also isolated. TOMOV DNA-A contains the AC1
XX XX
XX gene (see AAT93294) that must be expressed for efficient replication of
XX XX
XX DNA-A and DNA-B. The invention involves production of transgenic plants
XX XX
XX containing DNA comprising AC1 or CI wild-type or mutant sequences that
XX XX
XX negatively interfere in trans with geminiviral replication during
XX XX
XX infection. Such transgenic plants are resistant to viral infection.
XX XX
XX (updated on 17-OCT-2003 to standardise OS field)
XX XX
SQ Sequence 2602 BP; 671 A; 561 C; 586 G; 784 T; 0 U; 0 Other;
  
```

Query Match 96.1%; Score 1040.8; DB 2; Length 2602;
 Best Local Similarity 98.0%; Pred. No. 0;
 Matches 1054; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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QY 8 CACCAAGAAATTTAGAGTTCAAGTCAAGAACTATTTCTTAATCTATCCAGTGTCTC 67
  
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Db      2602 CACCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTCCTTATCCAGAGTCTCTT 2543
QY      68 TATCTAAGAGAGAGACATTTCCCAATTTACAAAACTTAATATCCCGAGTCAACAGAAAT 127
Db      2542 TGTCTAAGAGAGAGACATTTCCCAATTTACAAAACTTAATATCCCGAGTCAATAGAAAT 2483
QY      128 TCATCAAAATTTGAGAGAGCTTCATGAAAATGGGGAACCTCATCTCCATGTGCTGTTC 187
Db      2482 TCATCAAAATTTGAGAGAGCTTCATGAAAATGGGGAACCTCATCTCCATGTGCTGTTC 2423
QY      188 AGTTGAGAGGTAAGTACCAATGACAGATAACAGATTCTTCGAGCTGGTCCGCCAACCC 247
Db      2422 AGTTGAGAGGTAAGTACCAATGACAGATAACAGATTCTTCGAGCTGGTCCGCCAACCC 2363
QY      248 GGTGAGACATTTCCATCCGAAATTTGAGAGAGCTTAATGAGCTCCGAGCTCAATCAT 307
Db      2362 GGTGAGACATTTCCATCCGAAATTTGAGAGAGCTTAATGAGCTCCGAGCTCAATCAT 2303
QY      308 ACATCGACAGAGAGAGATTCATTCGAAATGGGGAATTTCCAAATGAGCGGAGATCTG 367
Db      2302 ACATCGACAGAGAGAGATTCATTCGAAATGGGGAATTTCCAAATGAGCGGAGATCTG 2243
QY      368 CCAAGAGAGGCGAGAGCTGCTGCTAATGATTCATTCGAAATGGGGAATTTCCAAATGAGCGG 427
Db      2242 CCAAGAGAGGCGAGAGCTGCTGCTAATGATTCATTCGAAATGGGGAATTTCCAAATGAGCGG 2183
QY      428 TTCAATTCGCTTAGCGGTTCTAAGGAGAGAACCAACCAAAAGATTTGTATTCAAAATC 487
Db      2182 TTCAATTCGCTTAGCGGTTCTAAGGAGAGAACCAACCAAAAGATTTGTATTCAAAATC 2123
QY      488 ATTAACATCCGCTCTAATCTAGAACGATTTTCGAAAGGCTCCGGAACCTGGGTTCTC 547
Db      2122 ATTAACATCCGCTCTAATCTAGAACGATTTTCGAAAGGCTCCGGAACCTGGGTTCTC 2063
QY      548 CATTTCAAGTCTCTTCTTCTTCTAAGCTTCTGACGATGAGAGAGAGAGAGAGAGAGT 607
Db      2062 CATTTCAAGTCTCTTCTTCTTCTTCTAAGCTTCTGACGATGAGAGAGAGAGAGAGT 2003
QY      608 ATTTGGGAGCGGTGACGCTGCGCGCGCGAGTAGACCTGTATGATCATGCTGAGGGTG 667
Db      2002 ATTTGGGAGCGGTGACGCTGCGCGCGCGAGTAGACCTGTATGATCATGCTGAGGGTG 1943
QY      668 ATTTCAAGAGAGAGAGAGAGATGAGGCGGCTGTTAGGCCCACTAATCTATCTCATG 727
Db      1942 ATTTCAAGAGAGAGAGAGAGATGAGGCGGCTGTTAGGCCCACTAATCTATCTCATG 1883
QY      728 GACACCTAGACTTCAATGAGTTCGAGTCTTCTGAAATGATGTCAGTATTAAGTCAATG 787
Db      1882 GACACCTAGACTTCAATGAGTTCGAGTCTTCTGAAATGATGTCAGTATTAAGTCAATG 1823
QY      788 ACATCGACCGCATTTATCTAAGCTTAAGACCTGGAAGAAATGCTGGGGGCCAGAAAG 847
Db      1822 ACATCGACCGCATTTATCTAAGCTTAAGACCTGGAAGAAATGCTGGGGGCCAGAAAG 1763
QY      848 ATTGGCAATCAAAATTTGAGAGTTCGAGTCTTCTGAAATGATGTCAGTATTAAGTCCACAA 907
Db      1762 ATTGGCAATCAAAATTTGAGAGTTCGAGTCTTCTGAAATGATGTCAGTATTAAGTCCACAA 1703
QY      908 TCGTGTCTTCAATCTGCTGAGAGGCTCCAGCTTAAGAGATTTTGAACAAAGCAGAAA 967
Db      1702 TCGTGTCTTCAATCTGCTGAGAGGCTCCAGCTTAAGAGATTTTGAACAAAGCAGAAA 1643
QY      968 ATACAGGTCTAAGAACTGGAATGCAAGATGCAAGATCTTCAATCACCCTCAACAGCCCC 1583
Db      1642 ATACAGGTCTAAGAACTGGAATGCAAGATGCAAGATCTTCAATCACCCTCAACAGCCCC 1583
QY      1028 TCTATCAAGAGAGACACAGGCAAGCCAAAGAAAGGGCAATCAGAAAGCGCAGGGGT 1083
Db      1582 TCTATCAAGAGAGACACAGGCAAGCCAAAGAAAGGGCAATCAGAAAGCGCAGGGGT 1527

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RESULT 5
AAT93282

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ID      AAT93282 standard; DNA; 1169 BP.
XX
XX      AC      AAT93282;
XX
XX      DT      27-APR-1998 (first entry)
XX
XX      DE      Tomato mottle virus AC1 mutant Tomov-Acidim gene.
XX
XX      KM      Geminiivirus; Tomov-Acidim; AC1 gene; transdominant mutation;
XX      transgenic plant; disease resistance; ss; cyclic; circular.
XX
XX      OS      Tomato mottle virus; isolate Florida.
XX
XX      FH      Key
XX      CDS      44..1129
XX      FT      /*tag= a
XX
XX      PN      M09739110-A1.
XX
XX      PD      23-OCT-1997.
XX
XX      PF      15-APR-1997; 97MO-US006300.
XX
XX      PR      16-APR-1996; 96US-0015517P.
XX
XX      PA      (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX      (WISC) WISCONSIN ALUMNI RES FOUND.
XX
XX      PI      Scout UT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
XX
XX      DR      WPI; 1997-526447/48.
XX      P-PSDB; AAW34324.
XX
XX      PT      Transgenic plants expressing geminiivirus AC1 and CI wild-type and mutant
XX      PT      genes - have increased resistance to geminiivirus infection e.g. tomato
XX      PT      mottle virus, tomato yellow leaf curl virus or bean golden mosaic
XX      PT      geminiivirus.
XX
XX      PS      Claim 11; Page 60-62; 132p; English.
XX
XX      CC      This DNA sequence comprises a transdominant lethal mutant, designated
XX      CC      Tomov-Acidim, of the AC1 gene of tomato mottle virus (Tomov). It
XX      CC      encodes an AC1 protein (see AAW34324) that carries mutations in its NTP-
XX      CC      binding domains. The AC1 gene (see also AAT93294) must be expressed for
XX      CC      efficient replication of the two genomic components, DNA-A and DNA-B, of
XX      CC      the bipartite Tomov genome. The invention involves production of
XX      CC      transgenic plants containing DNA comprising geminiivirus AC1 or CI wild-
XX      CC      type or mutant sequences that negatively interfere in trans with
XX      CC      geminiiviral replication during infection. Such transgenic plants are
XX      CC      resistant to viral infection. The AC1/CI genes are especially from Tomov,
XX      CC      tomato yellow leaf curl virus or bean golden mosaic geminiivirus (see
XX      CC      AAT93282-93) and encode polypeptides (see AAW34324-35) that have
XX      CC      mutations in the highly conserved DNA-nicking and/or the NTP-binding
XX      CC      domains
XX
XX      SQ      Sequence 1169 BP; 363 A; 281 C; 255 G; 270 T; 0 U; 0 Other;
XX
XX      Query Match      95.9%; Score 1038.2; DB 2; Length 1169;
XX      Best Local Similarity 97.4%; Pred. No. 0;
XX      Matches 1055; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

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QY      1 ATGCCCCCAACCAAGAAATTTAGAGTTCAGTCAAGAACTAATTTCTTCACTAATCCCGAG 60
Db      44 ATGCCCCCAACCAAGAAATTTAGAGTTCAGTCAAGAACTAATTTCTTCACTAATCCCGAG 103
QY      61 TGTCTCTATCTAAGAGAGACATTTCCCAATTTCAAAAACCTAATATCCCGAGTCAAC 120
Db      104 TGTCTCTTGTCTAAGAGAGACATTTCCCAATTTCAAAAACCTAATATCCCGAGTCAAT 163
QY      121 AAGAAATTCATCAAAATTTGAGAGAGCTTCATGAAGATGGGGAACCTCATCTCATGTG 180
Db      164 AAGAAATTCATCAAAATTTGAGAGAGCTTCATGAAGATGGGGAACCTCATCTCATGTG 223

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QY 181 CTGTGTCAGTTGCAAGGTAAGTACCAATGCAAGATAAGATTCTTGCAGCTGTCTCC 240
Db 224 CTTGTTCAGTTGCAAGGTAAGTACCAATGCAAGATAAGATTCTTGCAGCTGTCTCC 283
QY 241 CCAACCCGGTGAAGACATTTTCATCCGAATATTCAGGAGGTAAATGAGCTCGAGCTC 300
Db 284 CCAACCCGGTGAAGACATTTTCATCCGAATATTCAGGAGGTAAATGAGCTCGAGCTC 343
QY 301 AAATCATCATGCAAGAGACGAGATGCAATTCGAATGGGAGATTTTCAATGACGGC 360
Db 344 AAATCGTACATGCAAGAGACGAGATGCAATTCGAATGGGAGATTTTCAATGACGGC 403
QY 361 AGATCTGCGAGAGAGGCGACAGCTGCTATGATGATTCATTTGGGAAAGCATTAATGCA 420
Db 404 AGATCTGCGAGAGAGGCGACAGCTGCTATGATGATTCATTTGGGAAAGCATTAATGCA 463
QY 421 GGTTCGGTTCATGCTGCTTACGCGTTCTAAGGAGAAACAACCAAAAGATTTTGTATTA 480
Db 464 AGTTGGTTCAATCGCTTACAGTTCTAAGGAGAAACAACCAAAAGATTTTGTATTA 523
QY 481 CAAATCATTAATCCTGCTTACCTTACAGAAATATTCGAAAGGCTCCGGAACCGTGG 540
Db 524 CAAATCATTAATCCTGCTTACCTTACAGAAATATTCGAAAGGCTCCGGAACCGTGG 583
QY 541 GTTCTCCATTTCAAGTCTCTTCTTCACTAAGCTCTGACGAGATGCAAGATGGGGCG 600
Db 584 GTTCTCCATTTCAAGTCTCTTCTTCACTAAGCTCTGACGAGATGCAAGATGGGGCG 643
QY 601 GATTAATTAATTCGGGACGGGTGACGCTGCGCGCGATAGACCTGTAAAGTATCATGTC 660
Db 644 GATTAATTAATTCGGGACGGGTGACGCTGCGCGCGATAGACCTGTAAAGTATCATGTC 703
QY 661 GAGGTGATTTAAAGACAGGGAAGACATGTGGGCGCGCTTAAAGCCCATTAATCAT 720
Db 704 GAGGTGATTTAAAGACAGGGAAGACATGTGGGCGCGCTTAAAGCCCATTAATCAT 763
QY 721 CTCAGTGAACCTAGACTTCAATGATGAGTCTTCTGAAATGATGTGCAATTAATGAGTC 780
Db 764 CTCAGTGAACCTAGACTTCAATGATGAGTCTTCTGAAATGATGTGCAATTAATGAGTC 823
QY 781 ATTGATGACATGCAACCGCATTTATCTAAAGCTAAAGACCTGGAAGAATGCTGGGGCC 840
Db 824 ATTAAATACATCGACCGCATTTATCTAAAGCTAAAGACCTGGAAGAATGCTGGGGCC 883
QY 841 CAGAAAGATTGGCAATCAAAATGCAATGACCTAAGCCAGTTCAATTAAGGCGGATC 900
Db 884 CAGAAAGATTGGCAATCAAAATGCAATGACCTAAGCCAGTTCAATTAAGGCGGATC 943
QY 901 CCAGCAATCGTCTTTGCAATCTGTGAGGGGTGCGAGCTATTAAGAAGTCTTGAACAA 960
Db 944 CCAGCAATCGTCTTTGCAATCTGTGAGGGGTGCGAGCTATTAAGAAGTCTTGAACAA 1003
QY 961 GCAGAAAATAGAGTCTTCAAGACTGCACTATCAAGAAATGCGATCTTATCAACCTCACA 1020
Db 1004 GCAGAAAATAGAGTCTTCAAGACTGCACTATCAAGAAATGCGATCTTATCAACCTCACA 1063
QY 1021 GCCCCCTCTTTCAGAGAGACACAGGCAAGCCAAAGAAAGGCAATCAGAAGCGCAG 1080
Db 1064 GCCCCCTCTTTCAGAGAGACACAGGCAAGCCAAAGAAAGGCAATCAGAAGCGCAG 1123
QY 1081 GGT 1083
Db 1124 GGT 1126

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RESULT 6
 AAT93285
 ID AAT93285 standard; DNA; 1166 BP.
 AC AAT93285;
 XX
 DT 27-APR-1998 (first entry)

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XX DE Tomato mottle virus AC1 mutant gene.
XX DE Geminivirus; ToMoV-Acid1m23; AC1 gene; transdominant mutation;
XX KM transgenic plant; disease resistance; ss; cyclic; circular.
XX OS Tomato mottle virus; isolate Florida.
XX OS Synthetic.
XX FH Key
XX FT CDS
XX FT 44..439
XX FT /*tag= a
XX PN M09739110-A1.
XX PD 23-OCT-1997.
XX 15-APR-1997; 97MO-US006300.
XX 16-APR-1996; 96US-0015517P.
XX PA (SEMT-) SEMINIS VEGETABLE SEEDS INC.
XX PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX PI Stout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
XX WPI: 1997-526447/48.
XX DR P-PSDB; AAM34327.
XX PT Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
XX PT genes - have increased resistance to geminivirus infection e.g. tomato
XX PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
XX PT geminivirus.
XX PS Claim 11; Page 72-73; 132pp; English.
XX CC This DNA sequence comprises a mutated AC1 gene of tomato mottle virus
XX CC (ToMoV). It carries an inserted 4-base Sau3A site that shifts the AC1
XX CC gene translation reading frame resulting in the expression of a truncated
XX CC AC1 protein (see AAM34327). The AC1 gene (see also AAT93294) must be
XX CC expressed for efficient replication of the two genomic components, DNA-A
XX CC and DNA-B, of the bipartite ToMoV genome. The invention involves
XX CC production of transgenic plants containing DNA comprising geminivirus AC1
XX CC or CI wild-type or mutant sequences that negatively interfere in trans
XX CC with geminiviral replication during infection. Such transgenic plants are
XX CC resistant to viral infection. The AC1/CI genes are especially from ToMoV,
XX CC tomato yellow leaf curl virus or bean golden mosaic geminivirus (see
XX CC AAT93282-93) and encode polypeptides (see AAM34324-35) that have
XX CC mutations in the highly conserved DNA-nicking and/or the NTP-binding
XX CC domains
XX SO Sequence 1166 BP; 361 A; 277 C; 260 G; 268 T; 0 U; 0 Other;

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Query Match 95.5%; Score 1033.8; DB 2; Length 1166;
 Best Local Similarity 97.6%; Pred. No. 0;
 Matches 1061; Conservative 0; Mismatches 22; Indels 4; Gaps 1;

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QY 1 ATGCCCCCACCAGAAAGAAATTTAGAGTCAAGTCAAGAAACATTTCTTAATCCCAAG 60
Db 44 ATGCCCCCACCAGAAAGAAATTTAGAGTCAAGTCAAGAAACATTTCTTAATCCCAAG 103
QY 61 TGCTCTATCTAAAGAAAGACCTTCCCAATTACAAAACCTAATACCCAGTCAAC 120
Db 104 TGCTCTTGTCTAAAGAAAGACCTTCCCAATTACAAAACCTAATACCCAGTCAAT 163
QY 121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAAATGAGGAAACCTCATCTTCATGTG 180
Db 164 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAAATGAGGAAACCTCATCTTCATGTG 223
QY 181 CTTGTTCAAGTTGCAAGGTAAGTACCAATGCAAGAAATACAGATTTCTTGACCTGTCTCC 240
Db 224 CTTGTTCAAGTTGCAAGGTAAGTACCAATGCAAGAAATACAGATTTCTTGACCTGTCTCC 283

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QY 721 CTCAGTGAACACCTAGACTTTCATGTCAGTCTTTCGATGATGATGTCAGTATTAAGTTC 780
Db 361 CTCAGTGAACACCTAGACTTTCATGTCAGTCTTTCGATGATGATGTCAGTATTAAGTTC 420
QY 781 ATTGATGACATCGACCGCATTTATCTAAAGCTGAAGCACTGGAAGAATTGCTGGGGCC 840
Db 421 ATTGATGACATCGACCGCATTTATCTAAAGCTGAAGCACTGGAAGAATTGCTGGGGCC 480
QY 841 CAGAAAGATTGGCATCAATTTGCAAGTACCGTAAAGCACTTCAAAATTTAAAGCGGAATC 900
Db 481 CAGAAAGATTGGCATCAATTTGCAAGTACCGTAAAGCACTTCAAAATTTAAAGCGGAATC 540
QY 901 CCAGCAATCGTCTTGAATCCGTGTAGGGGTCCAGCTATTAAGAGTTCTTAGACAA 960
Db 541 CCAGCAATCGTCTTGAATCCGTGTAGGGGTCCAGCTATTAAGAGTTCTTAGACAA 600
QY 961 GCAGAAATACAGGTCTCAAGACCTGACATCAAGATGCGATCTTCAACCCCTGACA 1020
Db 601 GCAGAAATACAGGTCTCAAGACCTGACATCAAGATGCGATCTTCAACCCCTGACA 660
QY 1021 GCGCCCTCTATCAAGAGACACACAGGCAAGCCAGAAACGGCAATCAGAAAGCGCAG 1080
Db 661 GCGCCCTCTATCAAGAGACACACAGGCAAGCCAGAAACGGCAATCAGAAAGCGCAG 720
QY 1081 GGT 1083
Db 721 GGT 723
```

RESULT 8
AAT93314
ID AAT93314 standard; DNA; 1183 BP.

AC AAT93314;
XX 17-OCT-2003 (revised)
DT 27-APR-1998 (first entry)
XX

DE Bean golden mosaic geminivirus CI open reading frame.

XX Geminiivirus; BGMV; CI gene; transdominant mutation; transgenic plant;
KM disease resistance; ss; cyclic; circular.
XX

OS Bean golden mosaic virus; type II isolate Guatemala.

XX
FH Key Location/Qualifiers
FT CDS 1..1062
PT /*tag= a

PN WO9739110-A1.

XX 23-OCT-1997.

PD 15-APR-1997; 97WO-US006300.

XX 16-APR-1996; 96US-0015517P.

XX (SEMT-) SEMINIS VEGETABLE SEEDS INC.

PA (WISC) WISCONSIN ALUMNI RES FOUND.

PI Scout JT, Lau HT, Hanson SF, Maxwell DP, Ahlquist PG;

XX WPI; 1997-526447/48.

DR P-PSDB; AAW34338.

XX Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
PT genes - have increased resistance to geminivirus infection e.g. tomato
PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
PT geminivirus.

XX Example 5; Page 100-102; 132pp; English.

CC This genomic DNA sequence includes the open reading frame (ORF) of the
CC wild-type CI gene of bean golden mosaic virus (BGMV), a geminivirus that
CC has a monopartite genome. The CI protein (see AAW34338) is required for
CC replication. The wild-type CI ORF was subjected to Kunkel mutagenesis
CC (see AAT93290-93). The invention involves production of transgenic plants
CC containing DNA comprising CI or AC1 wild-type or mutant sequences that
CC negatively interfere in trans with geminiviral replication during
CC infection. Such transgenic plants are resistant to viral infection. The
CC AC1/CI genes are especially from BGMV, tomato mottle virus or tomato
CC yellow leaf curl virus (see AAT93282-93) and encode polypeptides (see
CC AAW34324-35) that have mutations in the highly conserved DNA-nicking
CC domain and/or the NTP-binding domains. (Updated on 17-OCT-2003 to
CC standardise OS field)

XX Sequence 1183 BP; 372 A; 276 C; 248 G; 287 T; 0 U; 0 Other;

Query Match 64.3%; Score 696.2; DB 2; Length 1183;
Best Local Similarity 77.9%; Pred. No. 1.3e-210;
Matches 839; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

```
QY 1 ATGCCCCACCAAGAAATTTAGAGTCACTCAAAAGACTATTTCCCTACTATCCCCAG 60
Db 1 ATGCAACCACTCAAGAAATTTAGAGTCACTCAAAAGACTATTTCCCTACTATCCCTG 60
QY 61 TGCTCTATCTAAAGAAAGCACTTCCCAATTACAAACCTAATATCCAGTCAAC 120
Db 61 TGCCCTATCCGAAGAAAGAAAGTTCTTCCCACTTCAAGAAATTCATACAGCCAGCAAT 120
QY 121 AAGAAATTCATCAAAATTTGCAAGAGCTTCATGAATGAGGAACTCATTCATGTG 180
Db 121 AAAAAATTCATCAAAAGCTGTGAGGAACGTACAGAAATGTTGAACCTCATCTTCATGCG 180
QY 181 CTGTTCAGTTGCAAGGTAAGTACCAATGACGAATACAGATTCCTTCGACTGGTCC 240
Db 181 CTATTAATTCGAAGTAATTCGTGTCGCAAAATTAAGATTTGTCAGCTGGTATCC 240
QY 241 CCAACCCGTCAGACATTTCCATCCGAAATTTCCAGGAGCTAATCGACTCCGAGTCC 300
Db 241 TCACACAGTTCAGACCTTTCCATCCGAACTTCAGGAGCTAATCAAGTTCAGAGTCC 300
QY 301 AATATCATTCGACAAAGACGAGATTAATGATGAGGAGATTTCCAAATGACGCG 360
Db 301 AAGGCAATCATCGACAAAGATGAGTCAATGCAATGAGGAGACATTCACAGTCCAGCGC 360
QY 361 AGATCGCCAGAGAGGCGCAGCTGCTAATGATTCATATGAGGAAGATTAATGCA 420
Db 361 AGATCTGAAGAGAGGTCAGAGTCTGCAACGACTCATATGGAAGCAATTAAGCGCA 420
QY 421 GGTTCGTTCAATCTGCTTGAAGCGGTTCTAAGGGAAGAACCAACCAAGATTTGTATTA 480
Db 421 GATTCAATGATCTGCTTGAAGCGGTTCTAAGGGAAGAACCAACCAAGATTTGTATTA 480
QY 481 CAAATCATTAACATCGCTCTTAACCTTAGAAGAAATTTCCGAAAGGCTCCGGAACGTTG 540
Db 481 CAACATCAACAATCCGTTCTTAATCTGAAACGATCTTCTCAAAAGGCGGGAACCAATGG 540
QY 541 GTTCCTCATTTCAAGTCTCTTCTTCACTAAGTCTCTGACGAGATGAGAGTGGCG 600
Db 541 GTTCCTCATTTCCGTTGTCATCAATTAATGATGATGATGATGATGATGATGATGATG 600
QY 601 GATTAATTTTCGGAGCGGTGACGCTGCGCGCGGATAGACCTGTAGATCATCGTC 660
Db 601 GAGCACTATTTTCGGAGCGGTTCGCTGCGCGCGGCGGAAAGACCTATTAATCATCGTC 660
QY 661 GAGGCTATTCAGAACAGAGAAAGCAATGTGGCGGCTGCTTAGGCCCACTAATCAT 720
Db 661 GAAGGTATTCAGAACCGGAAAGACCAATGTGGGCTCTGTCATTAAGACCACTAATTAAT 720
QY 721 CTCAGTGAACACCTAGACTTTCATGTCAGTCTTTCGATGATGATGTCAGTATTAAGTTC 780
Db 721 TTGAGCGGTATTTGACTTTAATTCACGTTGCTAATTCACAGAGTGGAAATACAGATC 780
QY 781 ATTGATGACATCGACCGCATTTATCTAAAGCTGAAGCACTGGAAGAATTGCTGGGGCC 840
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|||||
Db 781 ATTGATGACATAAGCCCCATTAATTGTAAGTAAAGCATGGAAGAACTAATTGGGGCA 840
Qy 841 CAGAAAGATTGGCAATCAATAATTGCAAGTACGGTAAAGCAAGTTAAATTAAGCGGATC 900
Db 841 CAAAGAGACTGGCAATCTAATCTAATATATGAAAGCGGTTCAATTAAGAGAGAAAT 900
Qy 901 CCAGCAATGCTGCTTTGGCAATCTCTGGTGAAGGGTCCAGCATTAATAAGAGTTCTTAGACAA 960
Db 901 CCATCAATGCTGTTGGCAATCCAGGTAAGGGTTCCAGTATTAAGACTTCCTCGACAA 960
Qy 961 GCAGAAATTAACAGTCTCAAGAACTGACATTAACAAGATTCCTCAACACCTCACA 1020
Db 961 GAAGAAACCGAGCTTTACCAACATGACATTAATGCAATCTTCGACACCTCACA 1020
Qy 1021 GCGCCCTCTATCAAGAGACACAGGCAAGCCCAAGAAACGGGCAATCGAAGGCG 1077
Db 1021 GCGCCCTCTATCAAGAGACACAGGATTCGCCAAACGTAGAGCCATTGCTGAGCG 1077
RESULT 9
ID AAA94700 standard; DNA; 1651 BP.
AC AAA94700;
XX
XX 15-JAN-2001 (first entry)
XX PMRG 2288 35S-rep gene cassette.
XX
XX Geminiivirus; DNA-A; geminivirus replication inhibition; ac3 gene;
XX transgenic plant; antiviral; gene therapy; bean golden mosaic virus;
XX BGWV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CaMV; ds.
XX
XX Bean golden mosaic virus.
XX Cauliflower mosaic virus.
XX Alfalfa mosaic virus.
XX Synthetic.
XX
XX US6118048-A.
XX
XX 12-SEP-2000.
XX
XX 24-APR-1998; 98US-00065999.
XX
XX 25-APR-1997; 97US-0044925P.
XX
XX (WISC) WISCONSIN ALUMNI RES FOUND.
XX
XX Maxwell DP, Hanson SF;
XX
XX WPI, 2000-610861/58.
XX
XX Genetic construct comprising a mutant geminiviral rep gene, useful for
XX producing a plant resistant to geminiviral infection.
XX
XX Example; Col 15-16; 14p; English.
XX
XX The present sequence is a 35S-rep gene cassette comprising the rep gene
XX of bean golden mosaic virus (BGWV)-GA cloned downstream of the CaMV 35S
XX promoter and an alfalfa mosaic virus (AMV) leader sequence. The sequence
XX was integrated into pBSII-KS+ to produce a rep gene expression vector.
XX DNA-ticking domain mutations may be incorporated into rep gene to produce
XX a genetic construct that acts as a trans-dominant inhibitor of
XX geminiviral replication. When expressed in a plant cell, this inhibitor
XX is able to dramatically reduce replication of geminivirus. Genetic
XX constructs that include sequences containing a portion of the ac3 gene in
XX addition to the trans-dominant inhibitor exhibit increased efficiency and
XX broadened specificity of inhibition of geminiviral replication.
XX Geminiviruses are one of the greatest constraints on production of
XX important crops, including cassava, beans, cowpeas, peppers, tomatoes and
XX cotton. The effects of the virus can be overcome by using the genetic
XX construct

XX
SQ Sequence 1651 BP, 517 A, 393 C, 342 G, 399 T, 0 U, 0 Other;
Query Match 64.3%; Score 696.2; DB 3; Length 1651;
Best Local Similarity 77.9%; Pred. No. 1,6e-210;
Matches 839; Conservative 0; Mismatches 238; Indels 0; Gaps 0;
Qy 1 ATGCCCCCAACCAAGAAATTTAGAGTTCAAGTCAAGAACTATTCTTAATTCACG 60
Db 469 ATGCCACCACTCAAGATTTAGAGTTCAAGTCAAGAACTATTCTTAATTCACG 528
Qy 61 TGCTCTCTATCTTAAGAAAGAGACCTTCCCAATTCAAAACTTAATCCGAGTCAAC 120
Db 529 TGCTCTATACCAAGAAAGAGATTTCTTGGCACTTCAGAAAGATTCATAGCCAGAA 568
Qy 121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAATAATGGGGAACCTCATCTCATG 180
Db 589 AAAAAATTCATCAAAATCTGTAGAGAACGTCAAGAAATGTGAACCTCATCTTCATG 648
Qy 181 CTGTTCAGTTGAGAGTAATGACATGACAGATTAACAGATTCTTCCAGCTGCTCC 240
Db 649 CTATTCAAATTCGAAGTAATTCGTCTGACAAATAAAGATTTGTCACCTGATACC 708
Qy 241 CCAACCCGGTCAAGCATTTCCATCCGAATATTCAGGGAGCTAATCGAGCTCCGAGTC 300
Db 709 TCACAGAGTCAGACCTTTCATCCGAACATTCAGAGCTAATTCAGTTAGAGTTC 768
Qy 301 AATCATATCATGACACAGAGACGAGATACATGCAATGGGAGATTTCCAAATCGACGC 360
Db 769 AAGCATATCATGACAAAGATGAGATGACATGCAATGGGGAATTCGAAGTCGACGC 828
Qy 361 AGATCTGCCAGAGAGGCGACAGCTGCTGATGATTCATATGCGAAAGCATTAATGCA 420
Db 829 AGATCTGCAAGAGAGGTGACGAGTCTGCCACAGCTCATATGCAAAAGGATTAACGCA 888
Qy 421 GGTTCGGTTCAATCTGCTTAAAGGGTCTTAAGGGAAAGCAACCAAAAGATTTGATTA 480
Db 889 GATTCATTAATCTGCTTGAACAATATGAAAGAAACACGAAAGATTAAGTCTT 948
Qy 481 CAAATCATTAATCCGCTCTAATCTAGAACGAAATTTGCAAAAGGCTCCGAAACCGTGG 540
Db 949 CAACATCAACAATCGGTTCTAATCTGAAAGGATCTTGCTCAAAAGTCCGGAACCATGG 1008
Qy 541 GTTCTCCATTTCAAGTCTTCTTCACTAACGTTCTGACGAGATGCAAGATGGGCG 600
Db 1009 GTTCTCCATTTCCGTTGTCATCATTCATCAATGTTCCGGTGTGTAAGCAAGATGGGTT 1068
Qy 601 GATAATTAATTTGGGACGGGTGACGGTGGCGCGCGGATTAAGCTGTAAGTATCATGCTC 660
Db 1069 GACGACTAATTTGGAAAGGGTTCGGTGGCGCGCGGAAAGACCTTAATGATATCATGCTC 1128
Qy 661 GAGGTGATTCAGAAACAGGAGAAAGATGAGGCGGCTGCTTAAGGCCACATACTAT 720
Db 1129 GAAGGTGATTCAGAAACCGGAAGAACATGTGGGCTGTGCTAATTAAGAACACATAATAT 1188
Qy 721 CTCAGTGACACCTAGACTTCAATGTCGAGTCTTCTCGAATGATGCAATTAACGTC 780
Db 1189 TTGAGCGGTCATTTGACCTTAATTAATCAACGTCATATCCAAACGAGTGGAATCAACGTC 1248
Qy 781 ATTGATGACATGCGACCGCATTTATCTAAGCTAAGCACTGGAAGAAATTCGCGGGGCC 840
Db 1249 ATTGATGACATAAGCCCCATTAATTGTAAGTAAAGCATGGAAGAACTAATTGGGGCA 1308
Qy 841 CAGAAAGATTGGCAATCAATAATTGCAAGTACGGTAAAGCAAGTTAAATTAAGCGGATC 900
Db 1309 CAAAGAGACTGGCAATCTAATCTAATATATGAAAGCGGTTCAATTAAGAGAGAAAT 1368
Qy 901 CCAGCAATGCTGCTTTGGCAATCTCTGGTGAAGGGTCCAGCATTAATAAGAGTTCTTAGACAA 960
Db 1369 CCATCAATGCTGTTGGCAATCCAGGTAAGGGTTCAGATTAATAAGCTTCGACAA 1428
Qy 961 GCAGAAATTAACAGTCTCAAGAACTGACATCAAGATTCGATCAACCTCACA 1020

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Db      1429 GAAGAAAACCGAGCTTACACAACTGACTATTCATATGCGATCTTTCGTACCCCTCA 1488
QY      1021 GCCCCCCCTATCAAGAGACACAGGCAAGCAAGAAACGGGCATTCGAAGGCG 1077
Db      1489 GCCCCCTCTATCAAGACACACAGATTGCTCCAAACGTAGAGCACTGTGACG 1545

RESULT 10
AAA94703
ID      AAA94703 standard; DNA, 1894 BP.
XX
XX      AAA94703;
AC
XX      15-JAN-2001 (first entry)
DT
XX
DE      pTrep3deltaE/CX nucleotide sequence.
XX
XX      Geminiivirus; DNA-A; geminivirus replication inhibition; ac3 gene;
KM      transgenic plant; antiviral; gene therapy; ds.
XX
XX      Synthetic.
OS
XX      US6118048-A.
PN
XX      12-SEP-2000.
PD
XX      24-APR-1998; 98US-00065999.
PF
XX      25-APR-1997; 97US-0044925P.
PR
XX      (WISC ) WISCONSIN ALUMNI RES FOUND.
PA
XX      Maxwell DP, Hanson SF;
PI
XX      WPI; 2000-610861/58.
DR
XX
PT      Genetic construct comprising a mutant geminiviral rep gene, useful for
XX      producing a plant resistant to geminiviral infection.
XX
XX      Example; Col 19-22; 14pp; English.
PS
XX
XX      The present sequence is pTrep3deltaE/CX. It contains a mutated
CC      geminivirus rep gene sequence. Genetic constructs containing DNA-nicking
CC      domain mutants in the rep gene may be used as trans-dominant inhibitors
CC      of geminiviral replication. When expressed in a plant cell, these
CC      inhibitors are able to dramatically reduce replication of geminivirus.
CC      Genetic constructs that include sequences containing a portion of the ac3
CC      gene in addition to the trans-dominant inhibitor exhibit increased
CC      efficiency and broadened specificity of inhibition of geminiviral
CC      replication. Geminiviruses are one of the greatest constraints on
CC      production of important crops, including cassava, beans, cowpeas,
CC      peppers, tomatoes and cotton. The effects of the virus can be overcome by
CC      using the genetic construct
XX
XX      Sequence 1894 BP; 604 A; 421 C; 388 G; 481 T; 0 U; 0 Other;
SQ
XX
XX      Query Match      64.3%; Score 696.2; DB 3; Length 1894;
XX      Best Local Similarity 77.9%; Pred. No. 1.7e-210;
XX      Matches 839; Conservative 0; Mismatches 238; Indels 0; Gaps 0;
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Db      649 CTTATTCATTCGAAGGTAATTCGTCTGCACAAATTAAGATTGTCAGCTGTATCC 708
QY      241 CCAACCCGGTACACACTTTCATCCGAATATTCAGGAGCTAATAGAGCTCCGAGTC 300
Db      709 TCAACGAGGTGACACCTTTCATCCGACATTCAGGAGCTAATCAAGTTCAGAGTC 768
QY      301 AAATCATATCATGCAACAAGACGAGATATCATGATAGGAGATTCCTCAATGACGGC 360
Db      769 AAGGATATCATTCGACAAAGATGAGTCAATCGAATGGGGACATTCGAAGTCAGCGC 828
QY      361 AGATCTGCAGAGAGGCGACAGTCTGCTAATGATTCATATGCGAAGCATTAATGCA 420
Db      829 AGATCTGCAGAGAGGCTGACAGTCTGCCAAGCATATGCAAGGATTAAGCGCA 888
QY      421 GTTTCGTTCAATCTGCTTACGCGTTCATAGGGAAGAACCAAGATTTGTATTA 480
Db      889 GATTCAATTAATCTGCTTACCAATATTAAGGAAGAACCAAGATTCGTCCTT 948
QY      481 CAATATCATATACATCCGCTTAACCTTGAACGAATATTCGCAAGGCTCCGAAACGCTG 540
Db      949 CAACATCAACATCCGTTCTTAATCTGAAAGCATCTTCGTAAGTCCGGAACATGG 1008
QY      541 GTTCTTCATTCGAAGTCTCTTTCATCACTACGTTCTGACAGATGCAAGAAATGGCG 600
Db      1009 GTTCCTTCATTCGTTGCTCATCATCATCAATGTTCCGGTTGTTATGCAAGATGGGTT 1068
QY      601 GATTAATATTTCCGAGAGCGGTGACGTCGCCGCCCGGATAGACCTGTAATCATATGTC 660
Db      1069 GACGACTAATTCGGAAGGAGGTTCCGCTGCGCGCGGGAAGACCTAATGATCATGTC 1128
QY      661 GAGGATATTCGAAGAACGAGGAAGACGATGTGGCGCGTCTGATGAGCCGACATTAAT 720
Db      1129 GAAGGTATTCAGGAACCGGAAGACAAATGTGGCTGTGTCATTAGGACCAATTAAT 1188
QY      721 CTCAGTGAACCTAGACTTCAATGTGAGTCTTCTGAAATGATGTCAGTATACGTC 780
Db      1189 TTGAGCGGTATTTGACATTTAAATTCACGTGTATTCACGACGATGGAATACACGTC 1248
QY      781 ATTGATGACATCCGACCGGCTTAATCTTAAGCTTAAGACCTGGAAGATTCGTGGGCGC 840
Db      1249 ATTGATGACATTAAGCCCAATTAATTTGAAGTTAAAGCACTGGAAGAACTAATTTGGGCA 1308
QY      841 CAGAAATATTCGCAATCAATTCGAACTGTAAGCAGTTCGAATTAAGGCGGATC 900
Db      1309 CAAGAGACTGCGAATTAATCTGAATATGAAAGCGGTTCAATTAAGAGGATTA 1368
QY      901 CAGCAATGCTGCTTTCGAATCTGTGAGGGTCCAGCTATTAAGAGTTCTTAGACAA 960
Db      1369 CCAATCAATCGTGTGTCGAATCCAGGAGGAGTCCAGTTATTAAGACTTCCGACAAA 1428
QY      961 GCAGAAATACAGGTCTCAAGAACTGCAATCAAGAAATGGAATGCTTCATCACCCCTCA 1020
Db      1429 GAAGAAAACCGAGCTTACACAACTGACTATTCATATGCGATCTTTCGTACCCCTCA 1488
QY      1021 GCCCCCCCTATCAAGAGACACAGGCAAGCAAGAAACGGGCATTCGAAGGCG 1077
Db      1489 GCCCCCTCTATCAAGACACACAGATTGCTCCAAACGTAGAGCACTGTGACG 1545

RESULT 11
AAA94702
ID      AAA94702 standard; DNA, 2072 BP.
XX
XX      AAA94702;
AC
XX      15-JAN-2001 (first entry)
DT
XX
DE      pTrep3 nucleotide sequence.
XX
XX      Geminiivirus; DNA-A; geminivirus replication inhibition; ac3 gene;
KM      transgenic plant; antiviral; gene therapy; ds.
XX
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OS Synthetic.
 XX US6118048-A.
 PN 12-SEP-2000.
 PD XX
 PF 24-APR-1998; 98US-0006599.
 XX
 XX 25-APR-1997; 97US-0044925P.
 XX
 XX (WISC) WISCONSIN ALUMNI RES FOUND.
 PA Maxwell DP, Hanson SF;
 PI MPI; 2000-610861/58.
 DR
 XX Genetic construct comprising a mutant geminiviral rep gene, useful for
 PT producing a plant resistant to geminiviral infection.
 XX
 XX Example; Col 17-20; 14pp; English.
 PS
 XX The present sequence is pTrep23. It contains the wild type geminivirus
 CC rep gene sequence. Genetic constructs containing DNA-nicking domain
 CC mutants in the rep gene may be used as trans-dominant inhibitors of
 CC geminiviral replication. When expressed in a plant cell, these inhibitors
 CC are able to dramatically reduce replication of geminivirus. Genetic
 CC constructs that include sequences containing a portion of the ac3 gene in
 CC addition to the trans-dominant inhibitor exhibit increased efficiency and
 CC broadened specificity of inhibition of geminiviral replication.
 CC Geminiviruses are one of the greatest constraints on production of
 CC important crops, including cassava, beans, cowpeas, peppers, tomatoes and
 CC cotton. The effects of the virus can be overcome by using the genetic
 CC construct
 XX
 SQ Sequence 2072 BP; 661 A; 467 C; 421 G; 523 T; 0 U; 0 Other;
 Query Match 64.3%; Score 696.2; DB 3; Length 2072;
 Best Local Similarity 77.9%; Pred. No. 1.8e-210;
 Matches 839; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

DB 949 CAAATCACAACATCGCTTCTAATCTCGAAGCATTTCTGCTAAATGCGGAAACCATGG 1008
 QY 541 GTTCTCTCAATTTCAAGTCTTCTTCACTAAAGTCTGACGAGATGCGAATGGCGC 600
 DB 1009 GTTCTCTCAATTTCCGTTGTCATTCATTCATCAATGTTCCGGTTGTATGCAAGATGGGTT 1068
 QY 601 GATTAATTTTGGGAGCGGCTGACGCTGCGCGCGCGGATAGACCTGTAAATATATGCTC 660
 DB 1069 GACGACTAATTTGGAAGGGGTTCCGCTGCGCGCGCGGAAAGACTTAATAGTATCATGCTC 1128
 QY 661 GAGGCGATTTCAAGAACAGGAAAGAGATGGGGCGGCGGCTTAGGCCCATTAATCTAT 720
 DB 1129 GAAAGGATTCACGAACCGAAGACATATGAGGCTGTGATTAAGACCATTAATATAT 1188
 QY 721 CTCAGTGAACACCTAGACTTTCATATGTCGAGTCTTCTCGAATGATGTCAGTATTAACGTC 780
 DB 1189 TTGAGCGGCTCATTTGGAATTTAATTCACGTTTATTCACAGCATGGAATACAAAGTC 1248
 QY 781 ATTGATGACATGCGACCGGATTTCTTAAAGCTAAGCACTGGAAGATTTGCTGGGGCC 840
 DB 1249 ATTGATGACATTAAGCCCAATTAATTTGAAGTTAAAGCACTGGAAGAACTAATTTGGGGCA 1308
 QY 841 CAGAAAGATTGGCAATCAATTAATGCAAGTACGGTAAGCCAGTTCAATTAAGCGGAATC 900
 DB 1309 CAAAGGACTGGCAATCTAATCTAATTAATGAAACCGGTTCAATTAAGAGAGATA 1368
 QY 901 CCAGCATGCTGCTTTCATCTGCTGAGGGTGCAGCATTAAGAGTCTTACACAA 960
 DB 1369 CATCAATGCTGTGTGCAATTCAGGTGAGGGTTCAGTTTAAACCTTCGACAA 1428
 QY 961 GCGAATAATACAGGTCTCAAGAACTGACTATCAAGATGCGATTTCAACCTTCACA 1020
 DB 1429 GAAAGAAACCGAGCTTTACACAACTGACTATTAATGCGATCTTCGTCACCTCACA 1488
 QY 1021 GCCCCCTCTATCAAGAGACACAGGCAAGCAAGAAACGGGCAATCAAGAGGG 1077
 DB 1489 GCCCCTCTATCAAGACCAACACAGATTTGCCAAACGTAGACATTCGTGACG 1545

RESULT 12
 AAT933290
 ID AAT93290 standard; DNA; 1183 BP.
 XX
 AC AAT93290;
 XX
 DT 17-OCT-2003 (revised)
 DT 27-APR-1998 (first entry)
 XX
 DE Bean golden mosaic geminivirus CI mutant gene.
 XX
 KM Geminivirus; BGMV; CI gene; transdominant mutation; transgenic plant;
 KM disease resistance; ss; cyclic; circular.
 XX
 OS Bean golden mosaic virus; type II isolate Guatemala.
 XX
 XX
 FH Key Location/Qualifiers
 FT CDS 1..1062
 FT /tag= a
 XX
 PN MO9739110-A1.
 XX
 PD 23-OCT-1997.
 XX
 PF 15-APR-1997; 97MO-US006300.
 PF
 PR 16-APR-1996; 96US-0015517P.
 XX
 XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX
 PI Stout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;

DR WPI; 1997-526447/48.
 DR P-PSDB; AAM34332.
 XX Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
 PT genes - have increased resistance to geminivirus infection e.g. tomato
 PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
 PT geminivirus.
 XX
 PS Claim 13; Page 103-105; 132pp; English.
 XX This DNA sequence comprises construct BGAC190 that codes for a control
 CC mutant (see AAM34332) of the CI protein (see AAM34338) of bean golden
 CC mosaic virus (BGMV). It was obtained by Kunkel mutagenesis of the wild-
 CC type CI gene (see AAT9314). CI is required for replication. The
 CC invention involves production of transgenic plants containing DNA
 CC comprising geminivirus CI or AC1 wild-type or mutant sequences that
 CC negatively interfere in trans with geminiviral replication during
 CC infection. Such transgenic plants are resistant to viral infection. The
 CC AC1/CI genes are especially from BGWV, tomato mottle virus or tomato
 CC yellow leaf curl virus (see AAT9282-93) and encode polypeptides (see
 CC AAM34324-35) that have mutations in the highly conserved DNA-nicking
 CC and/or the NTP-binding domains. (Updated on 17-OCT-2003 to standardise OS
 CC field)
 CC
 XX
 SQ Sequence 1183 BP; 371 A; 277 C; 249 G; 286 T; 0 U; 0 Other;
 Query Match 64.1%; Score 694.6; DB 2; Length 1183;
 Best Local Similarity 77.8%; Pred. No. 4.3e-210;
 Matches 838; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

QY 1 ATGCCCCACCAAGAAATTTAGAGTCAAGTCAAGAACTATTTCTTACTATCCAG 60
 DB 1 ATGCGACCACTCAAGATTTAGAGTCAAGTCAAGAACTATTTCTTACTATCCAGT 60
 QY 61 TGGCTCTCTAATAAGAAAGCACTTTCCCAATTACAAAACCTAAATACCCAGTCAAC 120
 DB 61 TGGCCCTATACCGAAGAAAGAAAGTCTTTCGCACTTCAAGAAATTCAGACCGCAAT 120
 QY 121 AAGAAATTCATCAAAATTTGAGAGAGTTCATGAAATGGGAGAGTTCATTCCTCATGTG 180
 DB 121 AAAAAATTCATCAAAAGTCTGAGAGAGAGTTCATGAAATGGGAGAGTTCATTCCTCATGTG 180
 QY 181 CTTGTCAGTTCGAGAGTGAATGCAATGCAAGTCAAGTTCCTTGAAGTCTGCTCC 240
 DB 181 CTTATTCATTCGAGAGTGAATGCTGTGCAAAATTAAGATTTGTCGACTGTATCC 240
 QY 241 CCAACCCGGTCAAGCAATTTCCATCCGAATTTAGGAGCTAAATGAGCTCCGAGCTC 300
 DB 241 TCAACCGGTCAAGCACTTTCCATCCGAATTTAGGAGCTAAATGAGCTCCGAGCTC 300
 QY 301 AAATCATATCAGACGAGAGAGATGATGCAATGCAATGGGAGATTTCCAAATGACGGC 360
 DB 301 AAGGCATATCAGACGAGAGAGATGAGTCAATGCAATGGGAGATTTCCAAATGACGGC 360
 QY 361 AGATCTGCAAGAGAGAGAGAGAGTCTGCTAATGATTCATATGGGAAAGCATTAATGCA 420
 DB 361 AGATCTGCAAGAGAGAGAGAGAGTCTGCCAAGCATCATATGCAAAAGGCAATTAAGCA 420
 QY 421 GGTTCGGTCAATGCTGCTTAAGCGTTCTAAGGGAAGAAACCAAAAGATTTGTATTA 480
 DB 421 GATTCATTAATTAATGCTGCTTAAGCAATATTAAGGAAACCAACCGAAAGATTTAGTCTT 480
 QY 481 CAAATCATATCAATCGGCTTAACCTTAAGAAAGAAATTTCCGAAAGGCTCCGGAACGGTGG 540
 DB 481 CAACATCAATCAATCGGCTTCTAATCTGAACGAAATTTCTTCCAAAGTCCGGAACCAATGG 540
 QY 541 GTTCCTCATATTCAGATCTCTCTTTCTTAACCTTAAGCAAGATGCAAGATGGCG 600
 DB 541 GTTCCTCATATTCAGATCTCTCTTTCTTAACCTTAAGCAAGATGGCGT 600
 QY 601 GATTAATTAATTTCCGAGAGGCTGAGCGTCCCGCCGGAATGACTGTAAGTATATGTC 660
 DB 601 GAGCACTAATTTCCGAGAGGCTTCCGCTGCGCGCGGCAAGAAAGCACTAATTAATCATGTC 660

QY 661 GAGGTGATTCAGAAACAGGAGACGATGTGGGCGGTGCTTAAGGCCACATACTAT 720
 DB 661 GAAAGGATTCAGCAACGAGAGAAACAAATGTGGGCTGTGATTAAGACCAATATAT 720
 QY 721 CTCAGTGACACCTAGACTTAATGTCAGATCTTCTGATGATGTCAGATTAACGTC 780
 DB 721 TTGAGCGGTCAATTTGACCTTAATTCACGTGTCTATTCGAACGAGTGAATCAACGTC 780
 QY 781 ATTGATGACATCGCAGCGCATTTATCTAAGCTAAAGACTGAAAGAAATGCTGGGGCC 840
 DB 781 ATTGATGACATTAAGCCCAATTTATTTGAATTAAGCACTGAAAGAACTAATTTGGGCA 840
 QY 841 CAGAAAGATTTGGCAATCAATTAAGTCAAGTAAAGCACTGCAATCAATTAAGCGCAATC 900
 DB 841 CAAAGGACTGCAATTAATCTAATTAATGAAAGCGGTTCAATTAAGGAGATATA 900
 QY 901 CCAACAATCGTGTTCGCAATCTGTGAGAGGTCCAGCTAATAAGAGTCTTAAGACAAA 960
 DB 901 CCATCAATCGTGTGTCGCAATCCAGGTGAGGTTCCAGTTAATAAGACTTCCTGACAAA 960
 QY 961 GCGAATAATACAGTCTCAAGAACTGACATTAAGAAATGCAATCTTCAATCACTTCA 1020
 DB 961 GAAGAAACCGAGCTTACCAACTGACATTAATGCAATCTTCACTTCACTTCACTCA 1020
 QY 1021 GCCCCCTTATCAAGAGACACAGGCAAGCAAGAAAGGCAATCGAAGGCG 1077
 DB 1021 GCCCCCTTATCAAGACACACAGGATTCGCAAGCAATCGAAGCAATTCGTGAGC 1077

RESULT 13
 ID AAA94701 standard; DNA; 1651 BP.
 XX AAA94701;
 AC 15-JAN-2001 (first entry)
 DT
 XX
 DE pTrepN nucleotide sequence.
 XX
 XX Geminivirus; DNA-A; geminivirus replication inhibition; ac3 gene;
 KM transgenic plant; antiviral; gene therapy; bean golden mosaic virus;
 KM BGWV; alfalfa mosaic virus; AMV; cauliflower mosaic virus; CaMV; ds.
 OS
 OS Bean golden mosaic virus.
 OS Cauliflower mosaic virus.
 OS Alfalfa mosaic virus.
 OS Synthetic.
 XX
 XX US6118048-A.
 XX
 XX
 PD 12-SEP-2000.
 XX
 XX 24-APR-1998; 98US-0006599.
 PF
 XX 25-APR-1997; 97US-0044925P.
 PR
 XX (MISC) WISCONSIN ALUMNI RES FOUND.
 PA
 XX Maxwell DP, Hanson SF;
 PI
 XX
 DR WPI; 2000-610861/58.
 XX
 XX Genetic construct comprising a mutant geminiviral rep gene, useful for
 PT producing a plant resistant to geminiviral infection.
 PS
 XX Example; Col 17-18; 14pp; English.
 XX
 XX The present sequence is pTrepN, a vector containing a CaMV-35S promoter-
 CC driven rep gene derived from bean golden mosaic virus (BGWV)-GA. Site-
 CC directed mutagenesis was used to engineer an NcoI site in the start codon
 CC of the rep gene to facilitate cloning of DNA-nicking domain mutants. The
 CC resulting genetic constructs act as trans-dominant inhibitors of

CC geminiviral replication. When expressed in a plant cell, these inhibitors are able to dramatically reduce replication of geminivirus. Genetic constructs that include sequences containing a portion of the ac3 gene in addition to the trans-dominant inhibitor exhibit increased efficiency and CC broadened specificity of inhibition of geminiviral replication. CC Geminiviruses are one of the greatest constraints on production of CC important crops, including cassava, beans, cowpeas, peppers, tomatoes and CC cotton. The effects of the virus can be overcome by using the genetic CC construct.

XX Sequence 1651 BP; 517 A; 392 C; 343 G; 399 T; 0 U; 0 Other;

Query Match 64.1%; Score 694.6; DB 3; Length 1651;
Best Local Similarity 77.8%; Pred. No. 5.1e-210;
Matches 838; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

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QY 1 ATGCCCCCAAGAAATTTAGAGTCAAGCAATTTCTTAATCCAG 60
DB 469 ATGGCACACCTTAAAGATTAGATTCAAGTCAAAACCTATTCTCACTTCTCTGT 528
QY 61 TGGCTCTATCTAAGAGAGCACTTCCCAATTACAAACCTAATACCCAGTCAAC 120
DB 529 TGGCCTATACGAAAGAAAGATTCTTTCGCACTTCAAGATTATACAGCAGCAAT 588
QY 121 AAGAAATTCATCAAAATTTGCAAGAGCTTCATGAATAAGGGAACTCATCTCCATGTG 180
DB 589 AAAAAATTCATCAAAAGCTGTGAGAACTGACAGAGATGTGAACTCATCTTCATGCG 648
QY 181 CTGTTCAGTTCGAGAGTAAAGTACCAATGACGAAATAGATTCTTCAGCTGTCTCC 240
DB 649 CTATTATCAATTCAGAGTAAATTCGTCTGCAAAATTAAGATTGTTGACCTGTGATCC 708
QY 241 CCAACCCGCTGACACATTTCCATCCGAATATTCAAGGAGCTTAATGAGCTCCAGCTC 300
DB 709 TCAACAGGCTGACACCTTCCATCCGAATATTCAAGGAGCTTAATGAGCTCCAGCTC 768
QY 301 AATATCATCTGACAGAGAGCGAGATACATGAAATGGGAGATTTCCAAATCGAGCGC 360
DB 769 AAGGCAATACATCAACAAAGATGAGTCAATCGAAATGGGAGCAATTCCAAGTCCAGCGC 828
QY 361 AGATCTGCCAGAGAGGCGAGAGTCTGATATGATTCAATGAGGAAAGCATTAATGCA 420
DB 829 AGATCTGCCAGAGAGGCTGAGAGTCTGCAACGATCATATGCAAGGATTAAGCGCA 888
QY 421 GGTTCGATTCATCTGCTTACCGCTTCTAAGGAGAAACACCAAAAGATTTGTATTA 480
DB 889 GATTCAATGAATCTGCTTACCAATATTAAGGAGAAACACCGAAAGATTTGTATTA 948
QY 481 CAAATCATATACATCCGCTTAACTGAACGAATATTCGCAAAAGCTCCGAAACGCTGG 540
DB 949 CAACATCACAAATCCGTTCTAATCTCGAACGATCTTCTCAAAAGTCCGGAACCATGG 1008
QY 541 GTTCTCATATTAAGCTCTTCTTTCACTAAGCTTCTGACGAGATGACGAGATGGGCG 600
DB 1009 GTTCTCATATTAAGCTCTTCTTTCACTAAGCTTCTGACGAGATGAGGAGTT 1068
QY 601 GATATATATTTCCGAGAGCGGTGACGCTGCCCGCGAGATGACCTGTATGATCATGTC 660
DB 1069 GACGACATATTTCCGAGAGCGGTGACGCTGCCCGCGAGATGACCTGTATGATCATGTC 1128
QY 661 GAGGCTGATTCAGAAACAGGAGAGAGATGTGGCGGTGCTGTTAGGCCCACTAATAT 720
DB 1129 GAAGGATATTCAGAAACAGGAGAGAGATGTGGCGGTGCTGTTAGGCCCACTAATAT 1188
QY 721 CTCAGTGAACACCTAAGCTTCAATGCGAGTCTTTCGATGATGCGATGTAACGTC 780
DB 1189 TTACGCGGTATTTGACCTTAAATTCACGCTGTCTATTCACGACGATGGAATACAGCTC 1248
QY 781 ATTGATGACATCGCAACCGCATTTCTAAGCTAAGACATGGAAGATTTGCTGGGGCC 840
DB 1249 ATTGATGACATCGCAACCGCATTTCTAAGCTAAGACATGGAAGATTTGCTGGGGCA 1308
QY 841 CAGAAAGATTGGCAATCAATTCAGAGTACGATGAGCACTTCAAAATTAAGCGCAATC 900

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DB 1309 CAAAGACTGGAAATTAATCTTAATATGAAACCGGTTCAATTAAGAGAGATTA 1368
QY 901 CCAGCATGCTGCTTTCGAATCTGCTGAGGCTGCGAGCTATTAAGAGTTCTTACAAA 960
DB 1369 CCATCATGCTGTTGTTGCAATCCAGGTGAGGGTTCAGTTATTAAGACTTCTCGACAAA 1428
QY 961 GCAGAAATACAGGCTTCAAGAACTGAGCTATCAAGATGCGATCTTCATACCTTCACA 1020
DB 1429 GAAGAAACCGAGCTTTACACAACTGACTATTCATATGCGATCTTCGACCTTCACA 1488
QY 1021 GCGCCCTCTATCAAGAGACACAGCAGCAGCAAGAAACGGGCAATCAGAGGGG 1077
DB 1489 GCGCCCTCTATCAAGACACACACAGATTCGCAAACTGAGACCATTCGTGACG 1545

```

RESULT 14
AAT93291
ID AAT93291 standard; DNA; 1062 BP.

```

XX AAT93291;
AC 17-OCT-2003 (revised)
DT 27-APR-1998 (first entry)
XX DE Bean golden mosaic geminivirus CI mutant ORF BGAC221.
XX KM Geminivirus; BGWV; CI gene; transdominant mutation; transgenic plant;
XX disease resistance; ss; cyclic; circular.
XX OS Bean golden mosaic virus; type II isolate Guatemala.
XX PN WO9739110-A1.
XX PD 23-OCT-1997.
XX PF 15-APR-1997; 97MO-US006300.
XX PR 16-APR-1996; 96US-0015517P.
XX PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
XX (WISC) WISCONSIN ALUMNI RES FOUND.
XX PT Stout UT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
XX P-PSDB; AAW34333.
XX DR WPI; 1997-526447/48.
XX PT Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
XX genes - have increased resistance to geminivirus infection e.g. tomato
XX mottle virus, tomato yellow leaf curl virus or bean golden mosaic
XX geminivirus.
XX PS Claim 13; Page 107-109; 132pp; English.
XX CC This DNA sequence comprises construct BGAC221 that codes for a
XX transdominant lethal mutant (see AAW34333) of the CI protein (see
XX AAW34338) of bean golden mosaic virus (BGWV). It was obtained by Kunkei
XX mutagenesis of the wild-type CI gene (see AAT93314). CI is required for
XX replication. The invention involves production of transgenic plants
XX containing DNA comprising geminivirus CI or AC1 wild-type or mutant
XX sequences that negatively interfere in trans with geminiviral replication
XX during infection. Such transgenic plants are resistant to viral
XX infection. The AC1/CI genes are especially from BGWV, tomato mottle virus
XX or tomato yellow leaf curl virus (see AAT93282-93) and encode
XX polypeptides (see AAW3434-35) that have mutations in the highly
XX conserved DNA-nicking and/or the NTP-binding domains. (Updated on 17-OCT-
XX 2003 to standardise OS field)
XX SQ Sequence 1062 BP; 339 A; 245 C; 219 G; 259 T; 0 U; 0 Other;

```

Query Match 63.8%; Score 691.2; DB 2; Length 1062;
Best Local Similarity 78.4%; Pred. No. 4.9e-209;

Matches 828; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

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QY 1 ATGCCCCCACCAGAAATTTAGAGTTCAGTCAAAAGACTATTTCTTACTTATCCAG 60
DB 1 ATGCGACACACTCAAAAGATTAGAGTTCAGTCAAAAGACTATTTCTTACTTATCCAG 60
QY 61 TGCCTCTATCTAAAGAGAGCACTTCCCAATTTACAAAACCTAAATACCCAGTCAAC 120
DB 61 TGCCTCTATCTAAAGAGAGCACTTCCCAATTTACAAAACCTAAATACCCAGTCAAC 120
QY 121 AAGAAATTCACAAATTTGACAGAGCTTCATGAAAATGGGAGCTCATCTTCATGTG 180
DB 121 AAGAAATTCACAAATTTGACAGAGCTTCATGAAAATGGGAGCTCATCTTCATGTG 180
QY 181 CTGTGTTAGTTCCAGAGTAACTACATGACGAAATACAGATCTTTCGACTGTCTCC 240
DB 181 CTGTGTTAGTTCCAGAGTAACTACATGACGAAATACAGATCTTTCGACTGTCTCC 240
QY 241 CCAACCCGTCAGACATTTCCATCCGAAATATTCAGGAGAGCTAAATGAGCTCCGAGTC 300
DB 241 TCAACCGTCAGACATTTCCATCCGAAATATTCAGGAGAGCTAAATGAGCTCCGAGTC 300
QY 301 AAATCATATCATCGAAGAGAGAGATGACATCGAATGGGAGATTTCCAAATGACGCG 360
DB 301 AAGGCATATCATCGAAGAGAGAGATGACATCGAATGGGAGATTTCCAAATGACGCG 360
QY 361 AGATCTGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
DB 361 AGATCTGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
QY 421 GGTTCGTTCAATCTGCTTACGCGTTCTAAAGGGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 GATTCAATGATATGCTGCTTACGCGTTCTAAAGGGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 CAAATCATATCATCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 CAAATCATATCATCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 GTTCCTCATATTCAGAGTCTTCTTCACTAAGCTTCTGACGAGATGGAGATGGGCG 600
DB 541 GTTCCTCATATTCAGAGTCTTCTTCACTAAGCTTCTGACGAGATGGAGATGGGCG 600
QY 601 GATATATTTATTCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 GATATATTTATTCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 GAGGCTATTTCCGAAAGGGGTCGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 GAGGCTATTTCCGAAAGGGGTCGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 CTGAGTGAACCTAGAGCTTCAATGTCAGTCTTCTGCAATGATGTGCAATTAAGCTC 780
DB 721 CTGAGTGAACCTAGAGCTTCAATGTCAGTCTTCTGCAATGATGTGCAATTAAGCTC 780
QY 781 ATTGATGACATCGACCGCATTTATCTAAAGCTAAAGAGCTGAAAGAGATTTGCTGGG 840
DB 781 ATTGATGACATCGACCGCATTTATCTAAAGCTAAAGAGCTGAAAGAGATTTGCTGGG 840
QY 841 CAGAAAGATTGGCAATCAAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 900
DB 841 CAGAAAGATTGGCAATCAAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 900
QY 901 CCAAGCATGCTGCTTCAATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 CCAAGCATGCTGCTTCAATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 GCAGAAATATCAGGCTCAAGAGATGCAATCAAGATGCAATCAAGATGCAATCAAGAT 1020
DB 961 GCAGAAATATCAGGCTCAAGAGATGCAATCAAGATGCAATCAAGATGCAATCAAGAT 1020
QY 1021 GCCCCCCCTTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1056
DB 1021 GCCCCCCCTTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1056

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RESULT 15
AAT93292
ID AAT93292 standard; DNA; 1062 BP.
XX
AC AAT93292;
XX
DT 17-OCT-2003 (revised)
DT 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus CI mutant ORF BGAC228.
XX
KW Geminivirus; BGWV; CI gene; transdominant mutation; transgenic plant;
KW disease resistance; ser; cyclic; circular.
XX
OS Bean golden mosaic virus; type II isolate Guatemala.
XX
PN W09739110-A1.
XX
PD 23-OCT-1997.
XX
PF 15-APR-1997; 97WO-US006300.
XX
PR 16-APR-1996; 96US-0015517P.
XX
PA (SEMT-) SEMINIS VEGETABLE SEEDS INC.
PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX
PI Scout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
XX
XX WPI: 1997-526447/48.
XX P-PSDB; AAM34334.
XX
PT Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
PT genes - have increased resistance to geminivirus infection e.g. tomato
PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
PT geminivirus.
XX
PS Claim 13; Page 111-112; 132pp; English.
XX
CC This DNA sequence comprises construct BGAC228 that codes for a
CC transdominant lethal mutant (see AAM34334) of the CI protein (see
CC AAM34338) of bean golden mosaic virus (BGWV). It was obtained by Kunke
CC mutagenesis of the wild-type CI gene (see AAT93314). CI is required for
CC replication. The invention involves production of transgenic plants
CC containing DNA comprising geminivirus CI or AC1 wild-type or mutant
CC sequences that negatively interfere in trans with geminiviral replication
CC during infection. Such transgenic plants are resistant to viral
CC infection. The AC1/CI genes are especially from BGWV, tomato mottle virus
CC or tomato yellow leaf curl virus (see AAT93282-93) and encode
CC polypeptides (see AAM34324-35) that have mutations in the highly
CC conserved DNA-nicking and/or the NTP-binding domains. (Updated on 17-OCT-
CC 2003 to standardise OS field)
XX
SQ Sequence 1062 BP; 338 A; 247 C; 218 G; 259 T; 0 U; 0 Other;

Query Match 53.8%; Score 691.2; DB 2; Length 1062;
Best Local Similarity 78.4%; Pred. No. 4.9e-209;
Matches 828; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

```

QY 1 ATGCCCCCACCAGAAATTTAGAGTTCAGTCAAAAGACTATTTCTTACTTATCCAG 60
DB 1 ATGCGACACACTCAAAAGATTAGAGTTCAGTCAAAAGACTATTTCTTACTTATCCAG 60
QY 61 TGCCTCTATCTAAAGAGAGCACTTCCCAATTTACAAAACCTAAATACCCAGTCAAC 120
DB 61 TGCCTCTATCTAAAGAGAGCACTTCCCAATTTACAAAACCTAAATACCCAGTCAAC 120
QY 121 AAGAAATTCACAAATTTGACAGAGCTTCATGAAAATGGGAGCTCATCTTCATGTG 180
DB 121 AAGAAATTCACAAATTTGACAGAGCTTCATGAAAATGGGAGCTCATCTTCATGTG 180
QY 181 CTGTGTTAGTTCCAGAGTAACTACATGACGAAATACAGATCTTTCGACTGTCTCC 240
DB 181 CTGTGTTAGTTCCAGAGTAACTACATGACGAAATACAGATCTTTCGACTGTCTCC 240
QY 241 CCAACCCGTCAGACATTTCCATCCGAAATATTCAGGAGAGCTAAATGAGCTCCGAGTC 300
DB 241 TCAACCGTCAGACATTTCCATCCGAAATATTCAGGAGAGCTAAATGAGCTCCGAGTC 300
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QY 361 AGATCTGCCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420
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QY 421 GGTTCGTTCAATCTGCTTACGCGTTCTAAAGGGAGAGAGAGAGAGAGAGAGAGAG 480
DB 421 GATTCAATGATATGCTGCTTACGCGTTCTAAAGGGAGAGAGAGAGAGAGAGAGAGAG 480
QY 481 CAAATCATATCATCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
DB 481 CAAATCATATCATCGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 540
QY 541 GTTCCTCATATTCAGAGTCTTCTTCACTAAGCTTCTGACGAGATGGAGATGGGCG 600
DB 541 GTTCCTCATATTCAGAGTCTTCTTCACTAAGCTTCTGACGAGATGGAGATGGGCG 600
QY 601 GATATATTTATTCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
DB 601 GATATATTTATTCGGAGCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 660
QY 661 GAGGCTATTTCCGAAAGGGGTCGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAG 720
DB 661 GAGGCTATTTCCGAAAGGGGTCGCGCGCGCGCGAGAGAGAGAGAGAGAGAGAGAG 720
QY 721 CTGAGTGAACCTAGAGCTTCAATGTCAGTCTTCTGCAATGATGTGCAATTAAGCTC 780
DB 721 CTGAGTGAACCTAGAGCTTCAATGTCAGTCTTCTGCAATGATGTGCAATTAAGCTC 780
QY 781 ATTGATGACATCGACCGCATTTATCTAAAGCTAAAGAGCTGAAAGAGATTTGCTGGG 840
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DB 841 CAGAAAGATTGGCAATCAAAATGCAATGCAATGCAATGCAATGCAATGCAATGCAATG 900
QY 901 CCAAGCATGCTGCTTCAATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
DB 901 CCAAGCATGCTGCTTCAATCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 960
QY 961 GCAGAAATATCAGGCTCAAGAGATGCAATCAAGATGCAATCAAGATGCAATCAAGAT 1020
DB 961 GCAGAAATATCAGGCTCAAGAGATGCAATCAAGATGCAATCAAGATGCAATCAAGAT 1020
QY 1021 GCCCCCCCTTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1056
DB 1021 GCCCCCCCTTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1056

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OM nucleic acid - nucleic acid search, using sw model

Run on: December 4, 2004, 13:17:10 ; Search time 116 Seconds

(without alignments)
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Searched: 824507 seqs, 355394441 residues

Total number of hits satisfying chosen parameters: 1649014

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1047.8	96.7	1162	3	US-08-838-151A-1 Sequence 1, Appl
2	1044.6	96.5	1169	3	US-08-838-151A-5 Sequence 5, Appl
3	1043	96.3	1169	3	US-08-838-151A-7 Sequence 7, Appl
4	1040.8	96.1	1262	3	US-08-838-151A-17 Sequence 17, Appl
5	1039.8	96.0	1169	3	US-08-838-151A-3 Sequence 3, Appl
6	1033.8	95.5	1166	3	US-08-838-151A-13 Sequence 13, Appl
7	702.2	64.8	1246	3	US-08-838-151A-15 Sequence 15, Appl
8	696.2	64.3	1183	3	US-08-838-151A-43 Sequence 43, Appl
9	696.2	64.3	1651	3	US-09-065-999-5 Sequence 5, Appl
10	696.2	64.3	1894	3	US-09-065-999-8 Sequence 8, Appl
11	696.2	64.3	2072	3	US-09-065-999-7 Sequence 7, Appl
12	694.6	64.1	1183	3	US-08-838-151A-45 Sequence 45, Appl
13	694.6	64.1	1651	3	US-09-065-999-6 Sequence 6, Appl
14	691.2	63.8	1062	3	US-08-838-151A-48 Sequence 48, Appl
15	691.2	63.8	1062	3	US-08-838-151A-51 Sequence 51, Appl
16	689.6	63.7	1062	3	US-08-838-151A-54 Sequence 54, Appl
17	496	45.8	1148	3	US-08-809-103B-1 Sequence 1, Appl
18	494.4	45.7	1145	3	US-08-809-103B-7 Sequence 7, Appl
19	492.8	45.5	1150	3	US-08-809-103B-3 Sequence 3, Appl
20	492.8	45.5	1150	3	US-08-809-103B-5 Sequence 5, Appl
21	479.4	44.3	1145	3	US-08-838-151A-19 Sequence 19, Appl
22	479.4	44.3	1145	3	US-08-838-151A-23 Sequence 23, Appl
23	479.4	44.3	1145	3	US-08-838-151A-26 Sequence 26, Appl
24	477.8	44.1	1145	3	US-08-838-151A-29 Sequence 29, Appl
25	418.4	38.6	1403	3	US-08-838-151A-59 Sequence 59, Appl
26	246.6	22.8	1403	3	US-08-838-151A-60 Sequence 60, Appl
27	185.2	17.1	780	3	US-08-838-151A-61 Sequence 61, Appl

28	47.2	4.4	517	4	US-09-936-552A-2 Sequence 2, Appl
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30	43.8	4.0	198	3	US-08-838-151A-57 Sequence 57, Appl
31	40.4	3.7	7218	1	US-08-232-463-14 Sequence 14, Appl
32	39.6	3.7	1110	3	US-09-414-276-2 Sequence 2, Appl
33	36.8	3.4	10236	3	US-09-453-702B-240 Sequence 240, Appl
34	34.2	3.2	784	2	US-08-750-654-1 Sequence 1, Appl
35	34.2	3.2	1141	4	US-09-806-708B-22 Sequence 22, Appl
36	34	3.1	3030	4	US-09-693-146-3 Sequence 3, Appl
37	33.6	3.1	832	4	US-09-621-976-2813 Sequence 2813, Appl
38	33.6	3.1	6268	4	US-09-566-921-57 Sequence 57, Appl
39	33.6	3.1	74962	4	US-09-685-853A-3 Sequence 3, Appl
40	33.4	3.1	389	4	US-09-621-976-8976 Sequence 8976, Appl
41	32.8	3.0	474	4	US-09-621-976-18033 Sequence 18033, Appl
42	32.8	3.0	1141	4	US-09-806-708B-22 Sequence 22, Appl
43	32.8	3.0	6407	2	US-08-616-844-7 Sequence 7, Appl
44	32.8	3.0	6407	2	US-08-599-654-7 Sequence 7, Appl
45	32.8	3.0	6407	3	US-08-944-868A-7 Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-08-838-151A-1
Sequence 1, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlgren, Paul
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1162 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemini Virus
INDIVIDUAL ISOLATE: Florida
FEATURE:
NAME/KEY: CDS

LOCATION: 44..1127
 PUBLICATION INFORMATION:
 AUTHORS: Gilbertson, RL
 AUTHORS: Hidayat, SH
 AUTHORS: Papiomatias, EJ
 AUTHORS: Rojas, MR
 AUTHORS: Hou, YM
 AUTHORS: Maxwell, DP
 TITLE: Pseudorecombination between the infectious
 TITLE: Cloned DNA components of tomato mottle and bean
 TITLE: dwarf mosaic geminiviruses.
 JOURNAL: Jour. General Virol.
 VOLUME: 74
 PAGES: 23-31
 DATE: 1993
 US-08-838-151A-1

Query Match 96.7%; Score 1047.8; DB 3; Length 1162;
 Best Local Similarity 98.0%; Pred. No. 0;
 Matches 1061; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 ATGCCCCCAGCAAGAAATTTAGAGTTCAGTCAAGAGCTATTCTTACTTATCCCGAG 60
 DB 44 ATGCCCCCAGCAAGAAATTTAGAGTTCAGTCAAGAGCTATTCTTACTTATCCCGAG 103
 QY 61 TGCTCTATCTAAGAAAGAGCCTTCCCAATTACAAAACCTAAATACCCAGTCAAC 120
 DB 104 TGCTCTATCTAAGAAAGAGCCTTCCCAATTACAAAACCTAAATACCCAGTCAAC 163
 QY 121 AAGAAATTCATCAAAATTTGCAAGAGCTTCATGAAAATGGGAACTCTATCTTCATGTG 180
 DB 164 AAGAAATTCATCAAAATTTGCAAGAGCTTCATGAAAATGGGAACTCTATCTTCATGTG 223
 QY 181 CTGTTCAGTTCGAAGGTAGTACCAATGCAAGAAATCAAGATTTCTTCGACCTGTCTCC 240
 DB 224 CTGTTCAGTTCGAAGGTAGTACCAATGCAAGAAATCAAGATTTCTTCGACCTGTCTCC 283
 QY 241 CCAACCCGTCAGACATTTCCATCCGAATATTGAGGAGCTAAATCGAGCTCCGACGTC 300
 DB 284 CCAACCCGTCAGACATTTCCATCCGAATATTGAGGAGCTAAATCGAGCTCCGACGTC 343
 QY 301 AAATCATATCATCGAAGAGAGGAGATATCAATCGAATGGGAGATTTCCAAATCGACGCG 360
 DB 344 AAATCATATCATCGAAGAGAGGAGATATCAATCGAATGGGAGATTTCCAAATCGACGCG 403
 QY 361 AGATTCGCCAGAGAGGCGCAGCATCTGCTAATGATTCATATGGAAGCATTTAAATGCA 420
 DB 404 AGATTCGCCAGAGAGGCGCAGCATCTGCTAATGATTCATATGGAAGCATTTAAATGCA 463
 QY 421 GGTTCGGTCAATCTGCTTAGCGGTTCTTAAGGGAAGAACCAAAAGATTTTGTATTA 480
 DB 464 AGTTCGGTCAATCTGCTTAGCGGTTCTTAAGGGAAGAACCAAAAGATTTTGTATTA 523
 QY 481 CAAATCATATCATCGCTCTTAACCTTAGAAAGAAATTTGCGAAAGGCTCCGGAACCGTGG 540
 DB 524 CAAATCATATCATCGCTCTTAACCTTAGAAAGAAATTTGCGAAAGGCTCCGGAACCGTGG 583
 QY 541 GTTCCTCATATTAAGTCTCTTCTTCACTAAGCTTCTTAAGGAGATTCGAGATGGGCG 600
 DB 584 GTTCCTCATATTAAGTCTCTTCTTCACTAAGCTTCTTAAGGAGATTCGAGATGGGCG 643
 QY 601 GATATATTTTCCGAGCGGCTGACGCTGCGCCGCGAGATAGACTGTAATATCATCTGTC 660
 DB 644 GATATATTTTCCGAGCGGCTGACGCTGCGCCGCGAGAGACTGTAATATCATCTGTC 703
 QY 661 GAGGGTGATTCAGAAACAGGGAAGACGATGTGGCGGCTGTTAGGCCACATTAATAT 720
 DB 704 GAGGGTGATTCAGAAACAGGGAAGACGATGTGGCGGCTGTTAGGCCACATTAATAT 763
 QY 721 CTGAGTGGAACCTAGACTTCATGCTGAGCTCTTCTCGAATATATGCGAGTATAAGTGC 780
 DB 764 CTGAGTGGAACCTAGACTTCATGCTGAGCTCTTCTCGAATATATGCGAGTATAAGTGC 823

QY 781 ATTGATGACATCGACCGCATTTATCTTAAGCTTAAGAGCATGGAAGAATTGCTGGGGCC 840
 DB 824 ATTGATGACATCGACCGCATTTATCTTAAGCTTAAGAGCATGGAAGAATTGCTGGGGCC 883
 QY 841 CAGAAAGATTGGCAATCAAAATTTGCAAGTACGTAAGCAGTTCAAATTAAGGCGGAATC 900
 DB 884 CAGAAAGATTGGCAATCAAAATTTGCAAGTACGTAAGCAGTTCAAATTAAGGCGGAATC 943
 QY 901 CCAGCAATCGTCTTTGCAATCTCTGTGAGAGGTGCCAGCTTAAGAAGTCTTAGACAAA 960
 DB 944 CCAGCAATCGTCTTTGCAATCTCTGTGAGAGGTGCCAGCTTAAGAAGTCTTAGACAAA 1003
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 DB 1064 GCCCCCTCTATCAAGAGACACACAGGCAAGCCCAAGAAACGCGCAATCAAGAGCGCAG 1123
 QY 1081 GGT 1083
 DB 1124 GGT 1126

RESULT 2

US-08-838-151A-5
 ; Sequence 5, Application US/08838151A
 ; Patent No. 6291743
 ; GENERAL INFORMATION:
 ; APPLICANT: Stout, John T
 ; APPLICANT: Lau, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSER: Dressler, Rocky, Milnamow & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838,151A
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mueller, Lisa V
 ; REGISTRATION NUMBER: 38,978
 ; REFERENCE/DOCKET NUMBER: SVS3801P0260
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-616-5400
 ; TELEFAX: 312-616-5460
 ; INFORMATION FOR SEQ ID NO: 5:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1169 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Tomato Mottle Geminivirus
 ; STRAIN: Florida


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QY 61 TGCTCTATCTAAGAGAGACCTTCCCAATTACAAAACCTAATACCAGTCAC 120
Db 104 TGCTCTATCTAAGAGAGACCTTCCCAATTACAAAACCTAATACCAGTCAC 163
QY 121 AAGAAATTCATCAAAATTTGAGAGAGCTTCATGAAAATGGGAACTCATCTCCATGTG 180
Db 164 AAGAAATTCATCAAAATTTGAGAGAGCTTCATGAAAATGGGAACTCATCTCCATGTG 223
QY 181 CTGTTCAGTTCCAGAGTAACTACCAATGCAAGAAATGCAATTTCTGCACTGGTCTCC 240
Db 224 CTGTTCAGTTCCAGAGTAACTACCAATGCAAGAAATGCAATTTCTGCACTGGTCTCC 283
QY 241 CCAACCCGTCAGACATTTCCATCCGATATTTCAGGAGCTAATGAGCTCCGAGCTC 300
Db 284 CCAACCCGTCAGACATTTCCATCCGATATTTCAGGAGCTAATGAGCTCCGAGCTC 343
QY 301 AAATCATACATCGACAGAGACGAGATACATCGAATGGGAGATTTCCAAATCGACGCG 360
Db 344 AAATCGTACATCGACAGAGACGAGATACATCGAATGGGAGATTTCCAGATCGACGCG 403
QY 361 AGATCTCCAGAGAGGCGCAGCACTCTGCTAATGATTCATATGCGAAAGCATTAATGCA 420
Db 404 AGATCTCCAGAGAGGCGCAGCACTCTGCTAATGATTCATATGCGAAAGCATTAATGCA 463
QY 421 GGTTCGGTCAATCTGCTTACGCGCTTCTAAGGAGAGAACCAACCAAAAGATTTGTATTA 480
Db 464 AGTTCGGTCAATCTGCTTACGCGCTTCTAAGGAGAGAACCAACCAAAAGATTTGTATTA 523
QY 481 CAAATCATACATCCGCTCTAACCCTAAGAAAGAAATTTCCGAAAGCTCCGAAACCGTGG 540
Db 524 CAAATCATACATCCGCTCTAACCCTAAGAAAGAAATTTCCGAAAGCTCCGAAACCGTGG 583
QY 541 GTTCCCTCATTTCAAGTCTCTTCTTCACTAAGCTTCTTCAAGAGATGCAAGAAATGGGCG 600
Db 584 GTTCCCTCATTTCAAGTCTCTTCTTCACTAAGCTTCTTCAAGAGATGCAAGAAATGGGCG 643
QY 601 GATTAATTTTGGGAGCGGTGACGCTGCGCGCGCGGATAGACCTGTAAGTATCATGCTC 660
Db 644 GATTAATTTTGGGAGCGGTGACGCTGCGCGCGCGGATAGACCTGTAAGTATCATGCTC 703
QY 661 GAGGGTATTCAGAGACAGGAGAGACGATGTGGGCGGTGGTAAAGCCCATTAATCTAT 720
Db 704 GAGGGTATTCAGAGACAGGAGAGACGATGTGGGCGGTGGTAAAGCCCATTAATCTAT 763
QY 721 CTGAGTGAACACCTAAGCTTCAATGCTGCAAGTCTTCTGCAATGATGTCAGATTAAGCTC 780
Db 764 CTGAGTGAACACCTAAGCTTCAATGCTGCAAGTCTTCTGCAATGATGTCAGATTAAGCTC 823
QY 781 ATTGATGACATCGACCGCATTTATCTAAGCTAAGACCTGGAAGAAATGCTGGGGGCC 840
Db 824 ATTGATGACATCGACCGCATTTATCTAAGCTAAGACCTGGAAGAAATGCTGGGGGCC 883
QY 841 CAGAAAGATTGGCAATCAAAATGCAAGTACGTAAGCCAGTTCATTAATTAAGGGGGAATC 900
Db 884 CAGAAAGATTGGCAATCAAAATGCAAGTACGTAAGCCAGTTCATTAATTAAGGGGGAATC 943
QY 901 CCGAGCATCTGCTTTGCAATCTCTGTAAGGAGGTCGCTAATAAGGTTCTTAAGACAA 960
Db 944 CCGAGCATCTGCTTTGCAATCTCTGTAAGGAGGTCGCTAATAAGGTTCTTAAGACAA 1003
QY 961 GCAGAAATACAGGCTCAAGAACTGACTATCAAGATGCAATCTTCATCAACCTCCACA 1020
Db 1004 GCAGAAATACAGGCTCAAGAACTGACTATCAAGATGCAATCTTCATCAACCTCCACA 1063
QY 1021 GCCCTCCCTCTATCAAGAGACACACAGCAAGCCAAAGAAACGGGCAATCAAGAGCGCAG 1080
Db 1064 GCCCTCCCTCTATCAAGAGACACACAGCAAGCCAAAGAAACGGGCAATCAAGAGCGCAG 1123
QY 1081 GGT 1083
Db 1124 GGT 1126

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RESULT 4
US-08-838-151A-17/c
; Sequence 17, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2602 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Tomato Mottle Geminivirus
; STRAIN: Florida
; US-08-838-151A-17

Query Match 96.1%; Score 1040.8; DB 3; Length 2602;
Best Local Similarity 98.0%; Pred. No. 0;
Matches 1054; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 8 CACCAAGAAATTTAGAGTTCAGTCAAGAACTAATTTCTAATCTATCCCAAGTCTCTC 67
Db 2602 CACCAAGAAATTTAGAGTTCAGTCAAGAACTAATTTCTAATCTATCCCAAGTCTCTC 2543
QY 68 TATCTAAGAGAGAGCACTTTCCCAATTACAAAACCTAATTAACCCAGTCAAGAAAT 127
Db 2542 TATCTAAGAGAGAGCACTTTCCCAATTACAAAACCTAATTAACCCAGTCAAGAAAT 2483
QY 128 TCATCAAAATTTGAGAGCTTCATGAATAATGGGGAACCTCATCTCCATGCTGTTTC 187
Db 2482 TCATCAAAATTTGAGAGCTTCATGAATAATGGGGAACCTCATCTCCATGCTGTTTC 2423
QY 188 AGTTCAAGAGTAACTACATGACAGAAATTAAGATTTCTGCACTGGTCTCCCAACC 247
Db 2422 AGTTCAAGAGTAACTACATGACAGAAATTAAGATTTCTGCACTGGTCTCCCAACC 2363
QY 248 GGTTCAGCATTTTCATCCGATATTTCAAGGAGGAGCTAATGAGCTCCGACGTCAATCAT 307
Db 2362 GGTTCAGCATTTTCATCCGATATTTCAAGGAGGAGCTAATGAGCTCCGACGTCAATCAT 2303

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QY 308 ACATCGACAGAGCGAGATGATCAATCGAATGGGAGATTTCGAATCGACGGCAGATCTG 367
DB 2302 ACATCGACAGAGCGAGATGATCAATCGAATGGGAGATTTCGAATCGACGGCAGATCTG 2243
QY 368 CCAGAGAGAGCGAGATGATCAATCGAATGGGAGATTTCGAATCGACGGCAGATCTG 427
DB 2242 CCAGAGAGAGCGAGATGATCAATCGAATGGGAGATTTCGAATCGACGGCAGATCTG 2183
QY 428 TTCAATCTGCTTACGAGTCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 487
DB 2182 TTCAATCTGCTTACGAGTCTTCAAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2123
QY 488 ATAAACATCGCTTAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 547
DB 2122 ATAAACATCGCTTAACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2063
QY 548 CATTGAGAGCTTCTTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 607
DB 2062 CATTGAGAGCTTCTTCACTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2003
QY 608 ATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 667
DB 2002 ATTTGGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1943
QY 668 ATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 727
DB 1942 ATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1883
QY 728 GACACCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 787
DB 1882 GACACCTAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1823
QY 788 ACATCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 847
DB 1822 ACATCGACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1763
QY 848 ATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 907
DB 1762 ATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1703
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DB 1702 TCGTGTCTTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1643
QY 968 ATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1027
DB 1642 ATACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1583
QY 1028 TCTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1083
DB 1582 TCTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1527

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RESULT 5
US-08-838-151A-3
Sequence 3, Application US/08838151A
Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Gemnivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.

```

? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1169 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOTHETICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Tomato Mottle Gemini Virus
? STRAIN: Florida
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 44..1127
? PUBLICATION INFORMATION:
? AUTHORS: Gilbertson, RL et al.
? TITLE: Pseudorecombination between the infectious
? TITLE: cloned DNA components of tomato mottle and bean
? TITLE: dwarf mosaic geminivirus
? JOURNAL: Journal of General Virology
? VOLUME: 74
? PAGES: 23-31
? DATE: 1993
? US-08-838-151A-3
?
? Query Match 96.0%; Score 1039.8; DB 3; Length 1169;
? Best Local Similarity 97.5%; Pred. No. 0;
? Matches 1056; Conservative 0; Mismatches 27; Indels 0; Gaps 0;
?
QY 1 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 60
DB 44 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 103
QY 61 TCGTCTTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
DB 104 TCGTCTTCTTAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 163
QY 121 AAGAAATTCATCAAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 180
DB 164 AAGAAATTCATCAAAATTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 223
QY 181 CTGTTCAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 240
DB 224 CTGTTCAGTTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 283
QY 241 CCAACCCGTCAGCAGATTTCCATCCGAATTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 300
DB 284 CCAACCCGTCAGCAGATTTCCATCCGAATTTTCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 343
QY 301 AATTCATCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 360
DB 344 AATTCATCATTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 403
QY 361 AGATCTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 420

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404 AGATCTCCAGAGAGGCGCAGCACTGTCTATGATTCATATGCGAAAGCGTTAATGCA 463
421 GGTTCGGTTCATCTGCTTAAAGCGTCTTAAGGAAACCAACCAAAAGATTTGTATTA 480
464 AGTTCGGTTCATCTGCTTAAAGCGTCTTAAGGAAACCAACCAAAAGATTTGTATTA 523
481 CAAATGATTAACCCGCTCTAAGCAATGATTTCCGAAAGGCTCCGGAACCGTGG 540
524 CAAATGATTAACCCGCTCTAAGCAATGATTTCCGAAAGGCTCCGGAACCGTGG 583
541 GTTCTCCATTCATCAAGTCTCTCTTCACTAAGCTTCTGAGATGCAAGAAATGGCGG 600
584 GTTCTCCATTCATCAAGTCTCTCTTCACTAAGCTTCTGAGATGCAAGAAATGGCGG 643
601 GATATTAATTTCCGGAAGGCGTGGCGCGCGCGATGAGCTGTAAGATATCATGTC 660
644 GATATTAATTTCCGGAAGGCGTGGCGCGCGCGATGAGCTGTAAGATATCATGTC 703
661 GAGGCTGATTCAGAAAGAGGAAAGAGATGAGCGCGCTGAGGCGCAATTAATCTAT 720
704 GAGGCTGATTCAGAAAGAGGAAAGAGATGAGCGCGCTGAGGCGCAATTAATCTAT 763
721 CTCAGTGAACAATACTTCAATGATGAGTCTTCTGAAATGATGCAATATACGTC 780
764 CTCAGTGAACAATACTTCAATGATGAGTCTTCTGAAATGATGCAATATACGTC 823
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824 ATTGATGACATTCGACGCGCAATTAAGTAAAGCACTGGAAGAATGCTGGGGGCGC 883
841 CAGAAAGATTCGCAATCAAAATTCGCAATGAGTAAAGCACTTCAAAATTAAGGCGGATC 900
884 CAGAAAGATTCGCAATCAAAATTCGCAATGAGTAAAGCACTTCAAAATTAAGGCGGATC 943
901 CCAGCAATTCGCTTTGCAATCTGCTGAGGAGTCCAGCTTAAGAAGTTCTTGAACAA 960
944 CCAGCAATTCGCTTTGCAATCTGCTGAGGAGTCCAGCTTAAGAAGTTCTTGAACAA 1003
961 GCAGAAATTCAGGCTCAAGAACTGACTATCAAGATGAGTCTTCAATCAACCTCCACA 1020
1004 GCAGAAATTCAGGCTCAAGAACTGACTATCAAGATGAGTCTTCAATCAACCTCCACA 1063
1021 GCCCCCCCTATCAAGAGAGACACAGGCAAGCCCAAGAAAGCGCAATCAAGAGCGCAG 1080
1064 GCCCCCCCTATCAAGAGAGACACAGGCAAGCCCAAGAAAGCGCAATCAAGAGCGCAG 1123
1081 GGT 1083
1124 GGT 1126

RESULT 6
US-08-838-151A-13
Sequence 13, Application US/08938151A

GENERAL INFORMATION:
Patent No. 6291743
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlgren, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiiviruses
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 1166 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Geminiiviruses
INDIVIDUAL ISOLATE: Florida
FEATURE:
NAME/KEY: CDS
LOCATION: 44..436
US-08-838-151A-13

Query Match 95.5%; Score 1033.8; DB 3; Length 1166;
Best Local Similarity 97.6%; Pred. No. 0;
Matches 1061; Conservative 0; Mismatches 22; Indels 4; Gaps 1;

1 ATGCCCCCAACCAAGAAATTTAAGTTCAGTCAAGAACTATTTCTTAATCCAG 60
44 ATGCCCCCAACCAAGAAATTTAAGTTCAGTCAAGAACTATTTCTTAATCCAG 103
61 TGCTCTCTATCTAAGAAAGAGAGCACTTCCCAATTAACCAAACTTAATCCAGTCAAC 120
104 TGCTCTCTATCTAAGAAAGAGAGCACTTCCCAATTAACCAAACTTAATCCAGTCAAC 163
121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAGATGGGAACTCATCTCCATGTG 180
164 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAGATGGGAACTCATCTCCATGTG 223
181 CTGTTCAAGTTCAAGGTAAGTACCAATGACAGATTAAGATTTCTGACCTGTCTCC 240
224 CTGTTCAAGTTCAAGGTAAGTACCAATGACAGATTAAGATTTCTGACCTGTCTCC 283
241 CCAACCCGTCACACATTTCCATCCGAATATTCAGGAGCTTAATCGAGCTCGAGTC 300
284 CCAACCCGTCACACATTTCCATCCGAATATTCAGGAGCTTAATCGAGCTCGAGTC 343
301 AATATCATCATCAAGAGAGAGAGATTAAGTGGGAGATTTCCAAATCGAGCGC 360
344 AATATCATCATCAAGAGAGAGAGATTAAGTGGGAGATTTCCAAATCGAGCGC 403
361 A---GATTCGCAAGAGAGAGAGAGATTAAGTGGGAGATTTCCAAATCGAGCGC 416
404 AGATCATCTGCGAGAGAGAGAGAGATTAAGTGGGAGATTTCCAAATCGAGCGC 463
417 TGAGGTTGGTTCATCTGCTTAAAGGAGTTCGAAAGAGAGAGAGATTTGAT 476
464 TGAGGTTGGTTCATCTGCTTAAAGGAGTTCGAAAGAGAGAGAGATTTGAT 523
477 ATTACAAATCATTAAGATCGCTCTAAGCAATGATTTCCGAAAGGCTCGGAGAC 536
524 ATTACAAATCATTAAGATCGCTCTAAGCAATGATTTCCGAAAGGCTCGGAGAC 583
537 GTGGTTCTCATTCATCAAGTCTCTTCTTCACTAAGCTTCTGAGAGATGAGAGATG 596

Db	584	GTGGGTTCTCCATTTCAAGTCTCTTTCTTCACTTAACGTTCCCTGACGAGATGACGAATG	643
Qy	597	GGGGGATTAATTAATTTGGGACGGGGGACGCTGCGCGCGCGGATATGACCTGTAAAGTATCAT	656
Db	644	GGCGGATTAATTAATTTGGGACGGGGTGACGTGCGCGCGCGGACGAGACCTGTAAAGTATCAT	703
Qy	657	CGTGAAGGATTAATTAAGAACGAGGAAACGATGTGGCGCGGTGCTTAAGGCCACATTA	716
Db	704	CGTGAAGGATTAATTAAGAACGAGGAAACGATGTGGCGCGGTGCTTAAGGCCACATTA	763
Qy	717	CTATCTCAGTGAACACCTTAAGCTTCAATGTGTGAGTCTTTCTCGAATGATGTGCAATTA	776
Db	764	CTATCTCAGTGAACACCTTAAGCTTCAATGTGTGAGTCTTTCTCGAATGATGTGCAATTA	823
Qy	777	CGTATTAATGATGACATTCGACCGCATTTATCTTAAAGCTTAAAGCACTGGAAGATTTGCTGG	836
Db	824	CGTATTAATGATGACATTCGACCGCATTTATCTTAAAGCTTAAAGCACTGGAAGATTTGCTAG	883
Qy	837	GGCCGAGAAAGATTGGCAATCAAAATTTGCAAGTACGGTAAGCACTTAATTAAGGCGG	896
Db	884	GGCCGAGAAAGATTGGCAATCAAAATTTGCAAGTACGGTAAGCACTTAATTAAGGCGG	943
Qy	897	AATCCGAGCAATCGTGCTTTTGCATTCCTGTGTGAGGTGCCGCTTAAGATTTCTTGA	956
Db	944	AATCCGAGCAATCGTGCTTTTGCATTCCTGTGTGAGGTGCCGCTTAAGATTTCTTGA	1003
Qy	957	CAAGGAGAAATTAACAGGTCTCAAGAACTGCACTTCAAGATGCGATCTTCATCACCT	1018
Db	1004	CAAGGAGAAATTAACAGGTCTTAAAGATCTGAATGTCAAGATGCGATCTTCATCACCT	1065
Qy	1017	CACGAGCCCCCTTATCAAGAGACACACAGGCAAGCCAAAGAGGCAATCGAAGGC	1078
Db	1064	CACGAGCCCCCTTATCAAGAGACACACAGGCAAGCCAAAGAGGCAATCGAAGGC	1123
Qy	1077	GCAGGCT 1083	
Db	1124	GCAGGCT 1130	
RESULT 7			
US-08-838-151A-15			
: Sequence 15, Application US/08838151A			
: Patent No. 6291743			
GENERAL INFORMATION:			
APPLICANT: Scout, John T			
APPLICANT: Lau, Hang T			
APPLICANT: Maxwell, Douglas			
APPLICANT: Ahlquist, Paul			
APPLICANT: Hanson, Steve			
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus			
TITLE OF INVENTION: Genes			
NUMBER OF SEQUENCES: 63			
CORRESPONDENCE ADDRESS:			
ADDRESSEE: Dressler, Rocky, Milnamow & Katz			
STREET: Two Prudential Plaza, Suite 4700			
CITY: Chicago			
STATE: Illinois			
COUNTRY: U.S.A.			
ZIP: 60601			
COMPUTER READABLE FORM:			
MEDIUM TYPE: Floppy disk			
COMPUTER: IBM PC compatible			
OPERATING SYSTEM: PC-DOS/MS-DOS			
SOFTWARE: Patentin Release #1.0, Version #1.30			
CURRENT APPLICATION DATA:			
APPLICATION NUMBER: US/08/838, 151A			
FILING DATE:			
CLASSIFICATION: 800			
ATTORNEY/AGENT INFORMATION:			
NAME: Mueller, Lisa V			
REGISTRATION NUMBER: 38,978			
REFERENCE/DOCKET NUMBER: SVS3801P0260			
TELECOMMUNICATION INFORMATION:			

	TELEPHONE:	312-616-5400	
	TELEFAX:	312-616-5460	
	INFORMATION FOR SEQ ID NO:	15:	
	SEQUENCE CHARACTERISTICS:		
	LENGTH:	1246 base pairs	
	TYPE:	nucleic acid	
	STRANDEDNESS:	single	
	TOPOLOGY:	circular	
	MOLECULE TYPE:	DNA (genomic)	
	HYPOTHETICAL:	NO	
	ANTI-SENSE:	NO	
	ORIGINAL SOURCE:		
	ORGANISM:	Tomato Mottle Geminivirus	
	STRAIN:	Florida	
	PUBLICATION INFORMATION:		
	AUTHORS:	Gilbertson, RL	
	AUTHORS:	Hidayat, SH	
	AUTHORS:	Papiliomatas, EJ	
	AUTHORS:	Rojas, MR	
	AUTHORS:	Hou, YM	
	AUTHORS:	Maxwell, DP	
	TITLE:	Pseudorecombination between the infectious	
	TITLE:	cloned DNA components of tomato mottle and bean	
	TITLE:	dwarf mosaic geminiviruses.	
	JOURNAL:	Journal of General Virology	
	VOLUME:	74	
	PAGES:	23-31	
	DATE:	1993	
	US-08-838-151A-15		
	Query Match	64.8%; Score 702.2; DB 3; Length 1246;	
	Best Local Similarity	98.2%; Pred. No. 1,4e-220;	
	Matches 710; Conservative 0; Mismatches 13; Indels 0; Gaps 0.		
Oy	361 AGATCTGCGACAGAGAGGGCCAGCAGCTCTGCTATGTATTGCAATGCGAAAGCATTAATAATGCA	420	
Db	1 AGATCTGCGACAGAGAGGGCCAGCAGCTCTGCTATGTATTGCAATGCGAAAGCATTAATAATGCA	60	
Oy	421 GGTTTCGGTTCATCTGCCTTAGCGGTTCTTAAAGGAACAACCMAAGATTTTGTAATTA	480	
Db	61 AGTTCGGTTCATCTGCCTTAGCGGTTCTTAAAGGAACAACAACCAAGATTTTGTAATTA	120	
Oy	481 CAAAATCATACATCCGCTCTAACCTGAAAGCAATATTGCAAAAGGCTCCGGAACCGGTG	540	
Db	121 CAAAATCATACATCCGCTCTAACCTGAAAGCAATATTGCAAAAGGCTCCGGAACCGGTG	180	
Oy	541 GTTCCCTCATTTCAAGTCTCTTCTTTCATCTAACGTTCTCTGACGAGATGCAGGAATGGGCG	600	
Db	181 GTTCCCTCATTTCAAGTCTCTTCTTTCATCTAACGTTCTCTGACGAGATGCAGGAATGGGCG	240	
Oy	601 GATAATTAATTTGCGGACGGGTGACGCTGCGGCCGCCGATAGACTCTGTAAGTATCATGCTC	660	
Db	241 GATAATTAATTTGCGGACGGGTGACGCTGCGGCCGCCGATAGACTCTGTAAGTATCATGCTC	300	
Oy	661 GAGGCTGATTCAGAACAAGGGAAGACGATGAGGCGCGGTGATTAGGCCCATTAATCTAT	720	
Db	301 GAGGCTGATTCAGAACAAGGGAAGACGATGAGGCGCGGTGATTAGGCCCATTAATCTAT	360	
Oy	721 CTCAGTGGACACCTAGACTTCAATGCTGAGTCTTCTTGAATGATGTGTCAGATTAACGTC	780	
Db	361 CTCAGTGGACACCTAGACTTCAATGCTGAGTCTTCTTGAATGATGTGTCAGATTAACGTC	420	
Oy	781 ATTGATGACATTCGACCGGCATTAATCTTAAAGCTTAAGCATCTGGAAGAAATTCCTGGGGCC	840	
Db	421 ATTGATGACATTCGACCGGCATTAATCTTAAAGCTTAAGCATCTGGAAGAAATTCCTGGGGCC	480	
Oy	841 CAGAAAGATTGGCAATCAAATTGGCAAGTACGCTGATAGCACAGTTCAAATTAAAGGCGCAATC	900	
Db	481 CAGAAAGATTGGCAATCAAANTGCAAGTACGCTGATAGCACAGTTCAAATTAAAGGCGCAATC	540	
Oy	901 CCAGCAATTCGCTCTTTGCAATCTCTGTGAGGGGTCCAGCTTAAAGAGTTCTTAGACAA	960	
Db	541 CCAGCAATTCGCTCTTTGCAATCTCTGTGAGGGGTCCAGCTTAAAGAGTTCTTAGACAA	600	

QY 961 GCAGAAATACAGCTCTCAAGACTGATCATCAAGATGATCTTCATCACCCCTGACA 1020
 Db 601 GCAGAAATACAGCTCTCAAGACTGATCATCAAGATGATCTTCATCACCCCTGACA 660
 QY 1021 GCCCCTCTATCAAGAGACACACAGCAAGCCAGAAACGGGCAATCAAGAGCGCAG 1080
 Db 661 GCCCCTCTATCAAGAGACACACAGCAAGCCAGAAACGGGCAATCAAGAGCGCAG 720
 QY 1081 GGT 1083
 Db 721 GGT 723
 RESULT 8
 US-08-838-151A-43
 ; Sequence 43, Application US/08838151A
 ; Patent No. 6291743
 ; GENERAL INFORMATION:
 ; APPLICANT: Stout, John T
 ; APPLICANT: Luu, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
 ; TITLE OF INVENTION: Gene
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Rockey, Milamow & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838,151A
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mueller, Lisa V
 ; REGISTRATION NUMBER: 38,978
 ; REFERENCE/DOCKET NUMBER: SYS3801P0260
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-616-5400
 ; TELEFAX: 312-616-5460
 ; INFORMATION FOR SEQ ID NO: 43:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1183 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Bean Golden Mosaic Gemminivirus
 ; STRAIN: Type II Isolates
 ; INDIVIDUAL ISOLATE: Guatemala
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 1..1059
 ; PUBLICATION INFORMATION:
 ; AUTHORS: Faria, JC
 ; AUTHORS: Gilbertson, RL
 ; AUTHORS: Hanson, SF
 ; AUTHORS: Morales, FJ
 ; AUTHORS: Ahlquist, P
 ; AUTHORS: Lomello, AO

; AUTHORS: Maxwell, D
 ; TITLE: Bean Golden Mosaic Gemminivirus Type II
 ; TITLE: Isolates from the Dominican Republic and
 ; TITLE: Guatemala: Nucleotide Sequences, Infectious
 ; TITLE: Pseudorecombinants, and Phylogenetic Relationships
 ; JOURNAL: Phycopathology
 ; VOLUME: 84
 ; ISSUE: 3
 ; PAGES: 321-329
 ; DATE: 1994
 ; US-08-838-151A-43
 Query Match 64.3%; Score 696.2; DB 3; Length 1183;
 Best Local Similarity 77.9%; Pred. No. 1,3e-218;
 Matches 839; Conservative 0; Mismatches 238; Indels 0; Gaps 0;
 QY 1 ATGCCCCCAACCAAGAAATTTAGAGTTCACTCAAGAACTATTTCTTAATCCCAAG 60
 Db 1 ATGCCACCACTCAAGAAATTTAGAGTTCACTCAAGAACTATTTCTTAATCCCAAG 60
 QY 61 TGCTCTCTATCTAAGAGAGAGACCTTCCCATTTACAAACCTTAATACCCAGTCAAC 120
 Db 61 TGCCCTATACCGAAGAGAGAGTCTTTTGCACCTTCAGAAAGTTCATACAGCCAGCAAT 120
 QY 121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAATGGGGAACCTCATCTCATGTG 180
 Db 121 AAAAAATTCATCAAAAGTCTGTGAGAGACGTCAAGAAATGGTGAACCTCATCTCATGCG 180
 QY 181 CTTGTTCAAGTTGAGAGTAAGTACCAATGACAGATACAGATTCGATCTGCTGCTCC 240
 Db 181 CTTATTCATTCAGAGTAATTCGTCGACAAATTAAGATTTGCTGACCTGATATCC 240
 QY 241 CCAACCCGTCACACATTTCCATCCGAATTCAGGAGCTTAATGAGCTCCGACGTC 300
 Db 241 TCAACCAAGTCAGACCTTTTCATCCGACATTCAGGAGCTTAATGAGCTTCAGACGTC 300
 QY 301 AAATCATACATCGACAAAGAGAGATACATGAAATGGGAGATTTCCAAATCGACGGC 360
 Db 301 AAGGATACATCGACAAAGATGAGATGACAAATGGGAGATTTCCAAATCGACGGC 360
 QY 361 AGATCTGCCAGAGAGGCGACAGTCTGTAATGATTCATATGCGAAGCATTAATGCA 420
 Db 361 AGATCTGCCAGAGAGGCTGACAGTCTGCCACAGACTCATATCAAGGATTAACGCA 420
 QY 421 GGTTCGGTCAATCTGCTTAAGCGGTTCTAAGGGAAGAACACCAAAAGATTTGATTA 480
 Db 421 GATTCATTAATGATCTGCTTAAGCAATTAAGGGAAGAACACCAAAAGATTTGATTA 480
 QY 481 CAATATCATTAATCCGCTCTAAGACGATATTCGCAAAAGGCTCCGGAACCGTGG 540
 Db 481 CAATATCAATCCGCTCTAATCTGAAGGATCTTCTCAAAAGTCCGGAACCAATGG 540
 QY 541 GTTCTCTCAATTCAGAGTCTCTTTCACTAAGCTTCGACAGATGACAGAAATGGCG 600
 Db 541 GTTCTCTCAATTCAGAGTCTCTTTCACTAAGCTTCGAGATTCGAGAAATGGGTT 600
 QY 601 GATTAATTTTGGGAGCGGCTGACGCTGCGCGCGGATGACCTGAATATCATGCTC 660
 Db 601 GAGACTAATTCGAGAGGCTTCGCTGCGCGCGGAGGAGGACTTAATGATATGCTC 660
 QY 661 GAGGCTGATTCAGAGACAGGAGAGAGATGAGGCGGCTGCTTAAGGCGGACCAATAT 720
 Db 661 GAGGCTGATTCAGAGACAGGAGAGAGATGAGGCGGCTGCTTAAGGCGGACCAATAT 720
 QY 721 CTGAGTGACACCTAGACTTCAATGCTGAGTCTTCTCGAATATGTCAGTAATACGTC 780
 Db 721 TTGAGGCTGATTCAGACTTCAATGCTGAGTCTTCTCGAATATGTCAGTAATACGTC 780
 QY 781 ATTGATGACATGCGACCGCATTTATCTAAGCTTAAGACACTGGAAGATTCGCTGGGGCC 840
 Db 781 ATTGATGACATTAAGCCCAATTTATTTGAAGTTAAAGACTGGAAGACTTAATTTGGGCA 840
 QY 841 CAGAAAGATTGGCAATCAATTCAGATGAGTGAAGCAAGTTCAAATTAAGCGGCAATC 900

DB 841 CAAAGGAGCTGGAAATCTAATCTAATATGAAAGCCGGTTAAATTAAGAGGAATA 900
QY 901 CCAGCAATGCTGCTTGAATCTGAGGGTGCAGATATAAGAGTTCTTAGACAAA 960
DB 901 CCATCAATGCTGTGTGCAATCCAGGTGAGGGTCCAGTTATAAGACTTCTCGACAAA 960
QY 961 GCAGAAATACAGGCTCAAGAACTGACTATCAAGATGCGATCTTCAATCACCCTACA 1020
DB 961 GAAGAAACCGAGCTTTACACAACTGACTATTCATATGCGATCTTCCGCACTTCACA 1020
QY 1021 GCCCCCCCTATCAAGAGACACAGGCAAGCCCAAGAAACGGGCATCAAGAGGG 1077
DB 1021 GCCCCCCCTATCAAGACACACAGAGATTGCCAAACGTAGAGCAATTCGTGACG 1077

RESULT 9
US-09-065-999-5
Sequence 5, Application US/09065999
Patent No. 6118048
GENERAL INFORMATION:
APPLICANT: Hanson, Stephen F.
APPLICANT: Maxwell, Douglas P.
TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
NUMBER OF INVENTIONS: 8
TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Quarles & Brady
STREET: One South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296, 94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1651 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-5

Query Match 64.3%; Score 696.2; DB 3; Length 1651;
Best Local Similarity 77.9%; Pred. No. 1.6e-218;
Matches 839; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

QY 181 CTGTTCAGTTCGAAGTAAGTACCAATCAGCAATTAAGATTCTTGCAGCTGGTCTCC 240
DB 649 CTATATCAATTCGAAGGTAAATTCCTGTCACAAAATTAAGATTGTTCCACCTGGATTC 708
QY 241 CCATCCCGGTTCAGCAATTTCCATCCGATATTTCAGGGAGCTTAAATCGAGCTCGAGTC 300
DB 709 TCAACCGGTTCAGCACTTTCATCCGAACATTCAGGGAGCTTAAATCAAGTTCAAGTC 768
QY 301 AAATCATATCAGACAGAGACGAGATACATATGAGTGGAGATTTCGAATTCAGACGCG 360
DB 769 AAGCGATATCAGACAAATATGAGATCAATATGAAATGGAGCAATTCAGTCCAGCGC 828
QY 361 AGATCTGCAAGAGAGCCAGAGCTGCTTAATGATTATATGCAAGCAATTAATGCA 420
DB 829 AGATCTGCAAGAGAGAGCTGCTGCAACGATCTGCAACGATCTATATGCAAGCAATTA 480
QY 421 GGTTCGCTTCATTCGCTTGAAGGTTCTAAGGGAAGAACCAAGATTGTTATTA 480
DB 889 GATTCAATTAATTCGCTTGAACATATTAAGAAAGAACCAAGATTGTTATTA 948
QY 481 CAAATCATATCAGATCCGCTCTAATCTAAGCAATATTCGAAAGGCTCCGAACCGTGG 540
DB 949 CAACATCAGACATCCGCTCTAATCTAATCTGCAAGGATCTTGTCAAGTGGCGGAAACAT 1008
QY 541 GTTCTCCATTTCAAGTCTCTTCTTCACTAAGCTTCTGACGATGCAAGATGGCGG 600
DB 1009 GTTCTCCATTTCCGTTGTCATCATTCATCAATGTTCCGTTGTTATGCAAGATGGGTT 1068
QY 601 GATTAATTTTGGGAGCGGGTGACCGGTGGCGCGGATGACCTGATGATCATGCTC 660
DB 1069 GAGACTATTTGGAAGGGGTTCCGCTGGCGCGGAAAGACATTAATGATCATGCTC 1128
QY 661 GAGGTGATTCAGAAACAGAGGAAGAGATGAGGCGCGTGGCTTGAAGCCACATTAAT 720
DB 1129 GAAGGTGATTCAGAAACAGAGGAAGAGATGAGGCGCGTGGCTTGAAGCCACATTAAT 1188
QY 721 CTGATGACACCTTAAGTCTTAATGAGTGGAGTCTTCAATGATGATGCAATTAAGT 780
DB 1189 TTGAGCGGTCAATTTGACCTTAATTCACGTTCTATTCGAAGCGAGTGAATTCACAG 1248
QY 781 ATTGATGATGACACCGGATTAATCTAAGCTTAAGCACTGGAAGAAATTCGCGGGGCG 840
DB 1249 ATTGATGATGACACCGGATTAATTTGAAGTTGAAGCACTGGAAGAAATTCGCGGGC 1308
QY 841 CAGAAAGATTGCAATCAATTTGCAAGTACGTTAAGCCAGTTCAATTAAGCGGAAATC 900
DB 1309 CAAAGAGCTGGCAATCTAATCTAATTAATGAAAGCCGTTCAATTAAGAGGAATA 1368
QY 901 CCAGCAATGCTGCTTGAATCTGAGGGTGCAGCTATTAAGATTCTTAGACAAA 960
DB 1369 CCATCAATGCTGTGTGCAATCCAGGTGAGGGTTCAGTTATAAGACTTCCCTCGACAAA 1428
QY 961 GCAGAAATACAGGCTCAAGAACTGAGTATCAAGATGCGATCTTCAATCACCCTACA 1020
DB 1429 GAAGAAACCGAGCTTTACACAACTGACTATTCATTAAGCAATTCCTGCACTCAC 1488
QY 1021 GCCCCCCCTATCAAGAGACACAGGCAAGCAAGAAACGGGCATCAAGAGGGG 1077
DB 1489 GCCCCCCCTATCAAGACACACAGAGATTGCCAAACGTAGAGCAATTCGTGAGAG 1545

RESULT 10
US-09-065-999-8
Sequence 8, Application US/09065999
Patent No. 6118048
GENERAL INFORMATION:
APPLICANT: Hanson, Stephen F.
APPLICANT: Maxwell, Douglas P.
TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
NUMBER OF INVENTIONS: 8
TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
CORRESPONDENCE ADDRESSES:

ADDRESSEE: Quarles & Brady
STREET: One South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296,94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1894 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-8

Query Match 64.3%; Score 696.2; DB 3; Length 1894;
Best Local Similarity 77.9%; Pred. No. 1,7e-218;
Matches 83; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

QY 1 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAACTATTCTTCTTATCCCGAG 60
DB 469 ATGCGACACCTCAAGATTAGAGTTCAGTCAAGAACTATTCTTCTTATCCCGAG 528
QY 61 TGCCTCTATCTAAGAAAGAACCTTCCCAATTACAAAACCTAATCCCGAGTAC 120
DB 529 TGCCTCTATCTAAGAAAGAACCTTCCCAATTACAAAACCTAATCCCGAGTAC 588
QY 121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAATAGGGAGCTCATCTCATGTG 180
DB 589 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAATAGGGAGCTCATCTCATGTG 648
QY 181 CTGCTCAGTTGGAAGGTAAAGTACCAATGACGAATACAGATTCTTGCACCTGGTCC 240
DB 649 CTGCTCAGTTGGAAGGTAAAGTACCAATGACGAATACAGATTCTTGCACCTGGTCC 708
QY 241 CCAACCGGTGACAGCAATTTCCATCCGAAATTCAGGAGCTAATGAGCTCCGAGTC 300
DB 709 TCAACCGGTGACAGCAATTTCCATCCGAAATTCAGGAGCTAATGAGCTCCGAGTC 768
QY 301 AATATCATATCGACAGAGACGAGATATCAATGAGTGGAGATTTCCAATGACGCG 360
DB 769 AATATCATATCGACAGAGACGAGATATCAATGAGTGGAGATTTCCAATGACGCG 828
QY 361 AGATTCGACAGAGAGCGACGAGCTGCTAATGATTCATATGCGAAGCAATTAATGCA 420
DB 829 AGATTCGACAGAGAGCGACGAGCTGCTAATGATTCATATGCGAAGCAATTAATGCA 480
QY 421 GATTCGCTCAATTCGCTTACGCGTTCATAGGAAAGAAACCAAAAGATTTGTATTA 480
DB 889 GATTCGCTCAATTCGCTTACGCGTTCATAGGAAAGAAACCAAAAGATTTGTATTA 948
QY 481 CAAATCATATACCGCTCTAATCTGAAGCAATTTTCGAAAGGCTCCGGAACGCTGG 540
DB 949 CAAATCATATACCGCTCTAATCTGAAGCAATTTTCGAAAGGCTCCGGAACGCTGG 1008
QY 541 GTTCTCTCATTTCAAGTCTCTTTCTTCACTAAGCTTCTGACGAGATGACGAATGGGCG 600

DB 1009 GTTCTCTCATTTCCGTTGTCATTCATCATATGTTCCGGTGTATGCAAGATGGGT 1068
QY 601 GATATATTTTGGGAGCGGTGAAGCTGCGCCCGCCGGAATGACCTGAATATCATGTC 660
DB 1069 GAGACATATTTGGAAGGGGTTCGCTGCGCGCGGCGGAAGACCTATTAATATCATGTC 1128
QY 661 GAGGTGATTCAGAAACAGAGGAAGACGATGCGCGGTGCTTTAGGCCCAATATAT 720
DB 1129 GAGGTGATTCAGAAACAGAGGAAGACGATGCGCGGTGCTTTAGGCCCAATATAT 1188
QY 721 CTGAGTGACACCTTAAGCTTCAATGCTGAGTCTTCTGAAATGATGCAATTAACGTC 780
DB 1189 TTGAGCGGTGATTTGACCTTAATTAATTCACGCTGCTATTCACCGAGTGAAATCAACGTC 1248
QY 781 ATGATGACATCCGACCGCATTCATTAAGCTTAAGACGTAAGAAATGCTGGGGGCC 840
DB 1249 ATGATGACATTAAGCCCAATTAATTAAGCTTAAGACGTAAGAAATGCTGGGGGCC 1308
QY 841 CAGAAATTTGCAATCAATTCAGTACGTAAGCAGTTCAGAAATTAAGCGCGAATC 900
DB 1309 CAGAAATTTGCAATCAATTCAGTACGTAAGCAGTTCAGAAATTAAGCGCGAATC 1368
QY 901 CAGCAATCGTCTTTCGCAATCTGCTGAGCGGTGCGACGTAATTAAGAGTTCTTAAGACAA 960
DB 1369 CAGCAATCGTCTTTCGCAATCTGCTGAGCGGTGCGACGTAATTAAGAGTTCTTCAACAA 1428
QY 961 GCAGAAATTCAGGTCTCAAGAACTGACATCAAGAAATGCAATTCATCAACCTGACA 1020
DB 1429 GAAGAAATTCAGGTCTCAAGAACTGACATCAAGAAATGCAATTCATCAACCTGACA 1488
QY 1021 GCCCCTCTATCAAGAGACAGACAGGCAAGCAAGAAAGCGGCAATCAGAAAGCG 1077
DB 1489 GCCCCTCTATCAAGAGACAGACAGGCAAGCAAGAAAGCGGCAATTCGTCGAGC 1545

RESULT 11
US-09-065-999-7
Sequence 7, Application US/09065999
Patent No. 6118048
GENERAL INFORMATION:
APPLICANT: Hanson, Stephen F.
TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles & Brady
STREET: One South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: US
ZIP: 53701-2113
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: PC-DOS/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/065,999
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Seay, Nicholas J.
REGISTRATION NUMBER: 27,386
REFERENCE/DOCKET NUMBER: 960296,94754
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608-251-5000
TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 2072 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-09-065-999-7

Query Match 64.1%; Score 696.2; DB 3; Length 2072;
Best Local Similarity 77.8%; Pred. No. 1.8e-218;
Matches 839; Conservative 0; Mismatches 238; Indels 0; Gaps 0;

```

QY 1 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAACTATTCTTAACTTATCCAG 60
DB 469 ATGCCACCACTCAAGATTAGAGTTGAGTCAAGAACTATTCTTAACTTATCCAG 528
QY 61 TGTCTCTATCTTAAAGAAAGACATTTCCCAATTCAGAACTTAATCCCAAGTCAAC 120
DB 529 TGCCTTATCCGAAAGAAAGAGTCTTTTCGCACTTCAGAAAGTATACAGCAGCAAT 588
QY 121 AAGAAATTCATCAAAATTTGACAGAGCTTCAGAAATTTGGGAGCTCATCTCAGT 180
DB 589 AAAAAATTCATCAAAATCTGTGAGAACTCAGAGAAAGTGTAACTTCACTTCAATG 648
QY 181 CTGTTCAGTTCGAAAGTAAGTACCAATGACGAAATTAAGATTTCTTCACTGCTCC 240
DB 649 CTATTCAATTCGAAAGTAATTCGTCTGCAAAATTAAGATTTGCACTGCTGATCC 708
QY 241 CCAACCCCGTCAAGACATTTCCATCCGAATTTCAAGAGCTTAATCGAGCTCCAGCTC 300
DB 709 TCAACCCGCTCAAGACATTTCCATCCGAATTTCAAGAGCTTAATTCAGTTCAGAGCTC 768
QY 301 AATCATCATGACGACAGGACGAGATPACATGAAATGGGAGATTTCCAAATCGACGGC 360
DB 769 AAGCATACATGACAAAGTAAGTACATGAAATGGGAGATTTCCAAATCGACGGC 828
QY 361 AGATCTGCAAGAGAGGCGAGAGTCTGTATGATTCATATCGAAAGCATTTAAATGCA 420
DB 829 AGATCTGCAAGAGAGAGTCTGTGAGTCTGCAAGATTCATATCGAAAGCATTTAAATGCA 888
QY 421 GGTTCGTTCAATCTGCTTAAAGGCTTCTTAAAGGAAACCAAAATTTTGTATTA 480
DB 889 GATTCATTTGAATCTCTTGAACAAATTTGAAGAAACCAAAATTTTGTATTA 948
QY 481 CAAATCATPACATGCGCTTAACTTAAAGCAATTTGCAAAAGGCTCCGAAACGCTG 540
DB 949 CAAATCATPACATGCGCTTAACTTAAAGCAATTTGCAAAAGGCTCCGAAACGCTG 1008
QY 541 GTTCTCTCAATTCAGTCTCTTCTTCACTTAAAGTCTTGAAGATTCAGATGCGCG 600
DB 1009 GTTCTCTCAATTCAGTCTCTTCTTCACTTAAAGTCTTGAAGATTCAGATGCGCG 1068
QY 601 GATATTTATTTGGGACGGGTGACGCTGCGCGCGCGATGACCTGTAGTATCATCTGTC 660
DB 1069 GACGACTATTTTGGGAGGGGTGCGCTGCGCGCGCGCGAAAGACCTTATGATATCATCTGTC 1128
QY 661 GAGGGGATTTCAAGAACAGGAGAGAGATGTTGGGCGGTGCTTAAAGCCCACTAATCTAT 720
DB 1129 GAGGGGATTTCAAGAACAGGAGAGAGATGTTGGGCGGTGCTTAAAGCCCACTAATCTAT 1188
QY 721 CTCAGTGAACCTTAAAGTGTGAGTCTTCTGATGATGATGATGATGATGATGATGATG 780
DB 1189 TTTGAGGCGTCTTAAAGTGTGAGTCTTCTGATGATGATGATGATGATGATGATGATGATG 1248
QY 781 ATTGATGACATCGCAGCGCTTAAAGTGTGAGTCTTCTGATGATGATGATGATGATGATG 840
DB 1249 ATTGATGACATCGCAGCGCTTAAAGTGTGAGTCTTCTGATGATGATGATGATGATGATG 1308
QY 841 CAGAAAGATTTGCAATCAATTTGCAAGTACGTAAGCAGTCAATTTAAAGCCGCAATC 900
DB 1309 CAGAAAGATTTGCAATCAATTTGCAAGTACGTAAGCAGTCAATTTAAAGCCGCAATC 1368
QY 901 CAGCAATGCTGCTTTGCAATCTGTGAGAGGTCAGCACTTAAAGATTTCTTAAAGCAAA 960
DB 1369 CAGCAATGCTGCTTTGCAATCTGTGAGAGGTCAGCACTTAAAGATTTCTTAAAGCAAA 1428
QY 961 GCGAAATATACAGGTCTCAAGAACTGAGCTATCAAGAAATGCGATCTTCAATCAGCTCACA 1020

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DB 1429 GAAGAAACAGGACTTACACACTGAGTATTCATATGCAATCTTCTGACCTCACA 1488
QY 1021 GCCCCCCCTATCAAGAGACACACAGCAGCAAGAAACGGGCAATCAAGAGCG 1077
DB 1489 GCCCCCCCTATCAAGAGACACACAGCAGTTCGCAAGCTAGAGCATTCGTGACG 1545

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RESULT 12

US-08-838-151A-45
Sequence 45, Application US/08838151A
Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T
APPLICANT: Lau, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Anagnostis, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESS: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 45:

SEQUENCE CHARACTERISTICS:
LENGTH: 1183 base pairs
TYPE: nucleic acid
STRANDEDNESS: single

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

ORGANISM: Bean Golden Mosaic Geminiivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala

FEATURE:

NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-45

Query Match 64.1%; Score 694.6; DB 3; Length 1183;
Best Local Similarity 77.8%; Pred. No. 4.3e-218;
Matches 838; Conservative 0; Mismatches 239; Indels 0; Gaps 0;

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QY 1 ATGCCCCCAAGAAATTTAGAGTTCAGTCAAGAACTATTCTTAACTTATCCAG 60
DB 1 ATGCCACCACTCAAGATTAGAGTTGAGTCAAGAACTATTCTTAACTTATCCAG 60
QY 61 TGTCTCTATCTTAAAGAAAGACATTTCCCAATTCAGAACTTAATCCCAAGTCAAC 120
DB 61 TGTCTCTATCTTAAAGAAAGACATTTCCCAATTCAGAACTTAATCCCAAGTCAAC 120
QY 121 AAGAAATTCATCAAAATTTGACAGAGCTTCAGAAATTTGGGAGCTCATCTCAGT 180
DB 121 AAGAAATTCATCAAAATCTGTGAGAACTCAGAGAAAGTGTAACTTCACTTCAATG 180
QY 181 CTGTTCAGTTCGAAAGTAAGTACCAATGACGAAATTAAGATTTCTTCACTGCTCC 240
DB 181 CTATTCAATTCGAAAGTAATTCGTCTGCAAAATTAAGATTTGCACTGCTGATCC 240
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DB 361 AGATCTGCAAGAGAGAGTCTGTGAGTCTGCAAGATTCATATCGAAAGCATTTAAATGCA 420
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DB 841 CAGAAAGATTTGCAATCAATTTGCAAGTACGTAAGCAGTCAATTTAAAGCCGCAATC 900
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QY 961 GCGAAATATACAGGTCTCAAGAACTGAGCTATCAAGAAATGCGATCTTCAATCAGCTCACA 1020
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QY 181 CTGTTCAGTTCGAAGGTAAGTCAATGCAAGAAATGAGATTCCTTCAGCTGTCTCC 240
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QY 241 CCAACCCGCTCAGACATTTTCATCCGAATATTGAGGAGCTAAATGAGCTCCGAGCTC 300
DB 241 TCAACCAAGGTCAGACATTTTCATCCGAATATTGAGGAGCTAAATGAGCTCCGAGCTC 300
QY 301 AAATCATATTCGACAGAGGAGAGATATCAATGCAATGGGAGATTTCCAAATGAGCGC 360
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DB 1021 GCGCCCTCTATCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1077
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RESULT 13

US-09-065-999-6

; Sequence 6, Application US/09065999

; Patent No. 6118048

; GENERAL INFORMATION:

; APPLICANT: Hanson, Stephen F.

; APPLICANT: Maxwell, Douglas P.

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; TITLE OF INVENTION: TRANS-DOMINANT INHIBITION OF GEMINIVIRAL
; TITLE OF INVENTION: DNA REPLICATION BY GEMINIVIRUS REP GENE MUTANTS
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Charles & Brady
; STREET: One South Pinckney Street
; CITY: Madison
; STATE: WI
; COUNTRY: US
; ZIP: 53701-2113
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/065,999
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Seay, Nicholas J.
; REGISTRATION NUMBER: 27,386
; REFERENCE/DOCKET NUMBER: 960296, 94754
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-251-5000
; TELEFAX: 608-251-9166
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1651 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-09-065-999-6
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Query Match 64.1%; Score 694.6; DB 3; Length 1651;
Best Local Similarity 77.8%; Pred. No. 5.3e-218;
Matches 838; Conservative 0; Mismatches 239; Indels 0; Gaps 0;
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DB 529 TGCCCTATACCAAGAGAGAGATTTCTTGGCAACTTCAGAGATTCATACAGCAGAAAT 588
QY 121 AAGAAATTCACAAATTTGCAAGAGAGCTTCATGAAATGGGAGAGCTCATCTCATGTG 180
DB 589 AAAAAATTCACAAAGTCTGTGAGAGAGTCAAGAGATGAGTCAAGCTCATCTTCATGCG 648
QY 181 CTGTTCAGTTCGAAGGATGATGCAATGAGAGATTAAGATTTCTGCACTGTGCTCC 240
DB 649 CTATTCATTAATTCGAAGGATTAATTCGTGCAAAATTAAGATTTGTCAGCTGTGATCC 708
QY 241 CCAACCCGCTCAGACATTTTCATCCGAATATTGAGGAGACTAAATGAGCTCCGAGCTC 300
DB 709 TCAACCAAGTCAAGACCTTTTCATCCGAATATTGAGGAGACTAAATGAGCTCCGAGCTC 768
QY 301 AAATCATATTCGACAGAGGAGAGATTAATTCAGTGTGAGTGTGAGTGTGAGTGTGAG 360
DB 769 AAGGCAATATTCGACAGAGGAGAGATTAATTCAGTGTGAGTGTGAGTGTGAGTGTGAG 828
QY 361 AGATCTGCGAGAGAGGAGAGAGATTAATTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 420
DB 829 AGATCTGCGAGAGAGGAGAGAGATTAATTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 888
QY 421 GGTTCGCTCAATTCGCTTACGCGTTCCTAAGGGAAGAACCAAAAGATTTGTATTA 480
DB 889 GATTCAATTAATTCGCTTACGCGTTCCTAAGGGAAGAACCAAAAGATTTGTATTA 948
QY 481 CAAATCATATTCGACAGAGGAGAGATTAATTCAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 540
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Db 949 CAACATCACACATCCGTTCTAATCTGAAACGATCTTCTGCAAAAGTCCGGAACATGG 1008
 QY 541 GTTCTTCATTTCAAGTCTCTTTCTTCACTAAGCTTCTGACAGATGACAGAAATGGGCG 600
 Db 1009 GTTCTTCATTTCAAGTCTCTTTCTTCACTAAGCTTCTGACAGATGACAGAAATGGGCG 1068
 QY 601 GATATATTTTGGGAGCGGTGACGCTGCGCGCGCGCGGATAGACTGTATATATATGTC 660
 Db 1069 GACGACTATTTTGGGAGCGGTGACGCTGCGCGCGCGGATAGACTGTATATATGTC 1128
 QY 661 GAGGATGATTCAGAAACAGGAGAAAGCATGTGGGCGGCTGTTAGGCCACATTAAT 720
 Db 1129 GAGGATGATTCAGAAACAGGAGAAAGCATGTGGGCGGCTGTTAGGCCACATTAAT 1188
 QY 721 CTGAGTGACACCTAGACTTCAATGTCGAGTCTTCTGATGATGTCAGATTAACGTC 780
 Db 1189 TTGAGCGGTATTTGACCTTAAATTCAGTGTCTATTCCAACGAGTGAATACAACTC 1248
 QY 781 ATTGATGACATCCGACCGCATTTATCTAAAGCTAAGCATGGAAGAAATGCTGGGGCC 840
 Db 1249 ATTGATGACATCCGACCGCATTTATCTAAAGCTAAGCATGGAAGAAATGCTGGGGCC 1308
 QY 841 CAGAAAGATTTGGCAATCAAAATGCAAGTACGTTAAGCCAGTTCATTAATTAAGCGGATC 900
 Db 1309 CAGAAAGATTTGGCAATCAAAATGCAAGTACGTTAAGCCAGTTCATTAATTAAGCGGATC 1368
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 Db 1369 CCAAGCATCTGCTTTTGAATCTCTGATGAGGGTCCAGCTATAAAGATTCTTAGACAA 1428
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 Db 1429 GAAGAAATACAGCTCTCAAGAACTGACATATCAAGAAATGCAATCTTCAATCACTTACA 1488
 QY 1021 GCCCCTCTATCAAGAGACACACAGGCAAGCCCAAGAAACGGGCAATCAAGAGGCG 1077
 Db 1489 GCCCCTCTATCAAGAGACACACAGGCAAGCCCAAGAAACGGGCAATCAAGAGGCG 1545

RESULT 14

US-08-838-151A-48

Sequence 48, Application US/08838151A

Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Luu, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Dressler, Rocky, Milnamow & Katz

STREET: Two Prudential Plaza, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,151A

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SVS3801P0260

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 48:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 1062 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: circular
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 ORIGINAL SOURCE:
 ORGANISM: Bean Golden Mosaic Geminivirus
 STRAIN: Type II
 INDIVIDUAL ISOLATE: Guatemala
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 1..1059
 US-08-838-151A-48

Query Match 63.8%; Score 691.2; DB 3; Length 1062;
 Best Local Similarity 78.4%; Pred. No. 5.4e-217;
 Matches 828; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

QY 1 ATGCCCCCACCAGAAATTTAGAGTTCAATCAAAAGACTATTTCTTAATCTTATCCAG 60
 Db 1 ATGCCCCCACCAGAAATTTAGAGTTCAATCAAAAGACTATTTCTTAATCTTATCCAG 60
 QY 61 TGCTCTCTATCTAAGAGAGACCTTCCCAATTAACAAACCTTAATCCAGTCAAC 120
 Db 61 TGCTCTCTATCTAAGAGAGACCTTCCCAATTAACAAACCTTAATCCAGTCAAC 120
 QY 121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAATGAGGAGCTCATCTCATGTG 180
 Db 121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAATGAGGAGCTCATCTCATGTG 180
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 Db 181 CTTGTTCACTTCAAGAGTATGTCATGACAGAAATTAAGATTTCTTCACTCTGTCTCC 240
 QY 241 CCAACCCGCTACGACATTTCCATCCGAATATTCAGGAGCTTAATCGAGCTCCGAGTC 300
 Db 241 CCAACCCGCTACGACATTTCCATCCGAATATTCAGGAGCTTAATCGAGCTCCGAGTC 300
 QY 301 AAATCATPACATCGACAGAGCGAGATPACATCGAATGAGGAGATTTCCAAATCGACGGC 360
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 QY 361 AGATCTGCAAGAGAGGAGCGAGCTGCTTAATGATTCATATGCGAAGATTAATGCA 420
 Db 361 AGATCTGCAAGAGAGGAGCGAGCTGCTTAATGATTCATATGCGAAGATTAATGCA 420
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 Db 541 GTTCTTCATTTCAAGTCTCTTTCTTCACTAAGTTCCTGACGAGATGCAAGAAATGGGCG 600
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 Db 661 GAGGATGATTCAGAAACAGGAGAAAGCATGTGGGCGGCTGTTAGGCCACATTAAT 720
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Db 721 TTGAGGGGTGATTTGGACCTTTAATTCACGTGTCTATCCAAAGCAGTGGAAATACAGTC 780
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Db 1021 GCCCCTCTATCAAGACACACAGGATTTGCCAA 1056

RESULT 15

US-08-838-151A-51
; Sequence 51, Application US/08838151A
; Patent No. 6291743
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 51:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1062 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEtical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bean Golden Mosaic Gemminivirus
; STRAIN: Type II
; INDIVIDUAL ISOLATE: Guatemala

FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1059
US-08-838-151A-51

Query Match 63.8%; Score 691.2; DB 3; Length 1062;
Best Local Similarity 78.4%; Pred. No. 5,4e-217;
Matches 828; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

Qy 1 ATGCCCCCACCAGAAATTTAGAGTTCAAGTCAAGAACTATTTCTTAATCTTATCCGAG 60
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Db 301 AAGGCATATCATCGACAAAGATGAGATGACATGCAATGAGGAGATTTCCAAATCGAGGC 360
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Db 361 AGATTCGACAGAGAGGCTGACAGCTGCTGCAAGATTCATTTGCGAAAGATTAATGCA 420
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Db 421 GATTCATTAATCTGCTTGAAGGAGGATTCGAAAGAGATTTGATTA 480
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Db 481 CAATCATATCATCGCTCTTAACTGAAGCAATATGCAAGAGCTCCGGAACCGTGG 540
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OM nucleic - nucleic search, using sw model

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(without alignments)
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Perfect score: 1083

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1047.8	96.7	1162	US-08-838-151A-1	Sequence 1, Appl1
2	1044.6	96.5	1169	US-08-838-151A-5	Sequence 5, Appl1
3	1043	96.3	1169	US-08-838-151A-7	Sequence 7, Appl1
4	1040.8	96.1	2602	US-08-838-151A-17	Sequence 17, Appl1
5	1039.8	96.0	1169	US-08-838-151A-3	Sequence 3, Appl1
6	1033.8	95.5	1166	US-08-838-151A-13	Sequence 13, Appl1
7	702.2	64.8	1246	US-08-838-151A-15	Sequence 15, Appl1
8	696.2	64.3	1183	US-08-838-151A-43	Sequence 43, Appl1
9	694.6	64.1	1183	US-08-838-151A-45	Sequence 45, Appl1
10	691.2	63.8	1062	US-08-838-151A-48	Sequence 48, Appl1
11	691.2	63.8	1062	US-08-838-151A-51	Sequence 51, Appl1
12	689.6	63.7	1062	US-08-838-151A-54	Sequence 54, Appl1

13	607.4	56.1	1056	18	US-10-633-850-79	Sequence 79, Appl1
14	607.4	56.1	1056	18	US-10-633-850-83	Sequence 83, Appl1
15	605.8	55.9	1056	18	US-10-633-850-50	Sequence 50, Appl1
16	605.8	55.9	1056	18	US-10-633-850-63	Sequence 63, Appl1
17	605.8	55.9	1056	18	US-10-633-850-91	Sequence 91, Appl1
18	605.8	55.9	1056	18	US-10-633-850-93	Sequence 93, Appl1
19	604.2	55.8	1056	18	US-10-633-850-81	Sequence 81, Appl1
20	604.2	55.8	1056	18	US-10-633-850-85	Sequence 85, Appl1
21	604.2	55.8	1056	18	US-10-633-850-95	Sequence 95, Appl1
22	604.2	55.8	1056	18	US-10-633-850-97	Sequence 97, Appl1
23	602.6	55.6	1056	18	US-10-633-850-61	Sequence 61, Appl1
24	602.6	55.6	1056	18	US-10-633-850-65	Sequence 65, Appl1
25	602.6	55.6	1056	18	US-10-633-850-75	Sequence 75, Appl1
26	602.6	55.6	1056	18	US-10-633-850-87	Sequence 87, Appl1
27	602.6	55.6	1056	18	US-10-633-850-89	Sequence 89, Appl1
28	601	55.5	1056	18	US-10-633-850-59	Sequence 59, Appl1
29	601	55.5	1056	18	US-10-633-850-67	Sequence 67, Appl1
30	601	55.5	1056	18	US-10-633-850-71	Sequence 71, Appl1
31	601	55.5	1056	18	US-10-633-850-73	Sequence 73, Appl1
32	601	55.5	1056	18	US-10-633-850-75	Sequence 75, Appl1
33	599.4	55.3	1056	18	US-10-633-850-51	Sequence 51, Appl1
34	599.4	55.3	1056	18	US-10-633-850-53	Sequence 53, Appl1
35	599.4	55.3	1056	18	US-10-633-850-55	Sequence 55, Appl1
36	596.2	55.1	1056	18	US-10-633-850-69	Sequence 69, Appl1
37	479.4	44.3	1145	8	US-08-838-151A-19	Sequence 19, Appl1
38	479.4	44.3	1145	8	US-08-838-151A-23	Sequence 23, Appl1
39	479.4	44.3	1145	8	US-08-838-151A-26	Sequence 26, Appl1
40	479.4	44.1	1145	8	US-08-838-151A-29	Sequence 29, Appl1
41	477.8	44.1	1047	18	US-10-633-850-110	Sequence 110, Appl1
42	445.6	41.1	1047	18	US-10-633-850-111	Sequence 111, Appl1
43	444	41.0	2744	8	US-08-838-151A-59	Sequence 59, Appl1
44	418.4	38.6	1403	8	US-08-838-151A-60	Sequence 60, Appl1
45	246.6	22.8				

ALIGNMENTS

RESULT 1
US-08-838-151A-1
; Sequence 1, Application US/08838151A
; Publication No. US20010011379A1
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSER: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38, 978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1162 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tomato Mottle Gemini Virus
; INDIVIDUAL ISOLATE: Florida
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 44..1127
; PUBLICATION INFORMATION:
; AUTHORS: Gilbertson, RL
; AUTHORS: Hidayat, SH
; AUTHORS: Paplomatae, EJ
; AUTHORS: Rojas, MR
; AUTHORS: Hou, YM
; AUTHORS: Maxwell, DP
; TITLE: Pseudorecombination between the infectious
; TITLE: cloned DNA components of tomato mottle and bean
; TITLE: dwarf mosaic geminiviruses.
; JOURNAL: Jour. General Virol.
; VOLUME: 74
; PAGES: 23-31
; DATE: 1993
US-08-838-151A-1

Query Match 96.7%; Score 1047.8; DB 8; Length 1162;
Best Local Similarity 98.0%; Pred. No. 2,4e-313;
Matches 1061; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

QY 1 ATGCCCCCAAGAAATTAGAGTTCAGTCAAGAAAGACTATTCTTAATATCCCGAG 60
DB 44 ATGCCCCCAAGAAATTAGAGTTCAGTCAAGAAAGACTATTCTTAATATCCCGAG 103
QY 61 TGTCTCTATCTAAAGAAAGACATTTCCTCAATTAACAAACCTTAATATCCCGAGTCAAC 120
DB 104 TGTCTCTATCTAAAGAAAGACATTTCCTCAATTAACAAACCTTAATATCCCGAGTCAAT 163
QY 121 AAGAAATTCATCAAAATTTGCAAGAGCTTCATTAATAATGGGAACTCTATTCATGTC 180
DB 164 AAGAAATTCATCAAAATTTGCAAGAGCTTCATTAATAATGGGAACTCTATTCATGTC 223
QY 181 CTGTTGAGTTCGAAGGTAAAGTACCAATGACAGCAATTAAGATTCCTGACCTGCTCC 240
DB 224 CTGTTGAGTTCGAAGGTAAAGTACCAATGACAGCAATTAAGATTCCTGACCTGCTCC 283
QY 241 CCAACCCGTCAGACATTTTCATCCGAATATTCAGGAGCTTAATGAGCTCCGACGTC 300
DB 284 CCAACCCGTCAGACATTTTCATCCGAATATTCAGGAGCTTAATGAGCTCCGACGTC 343
QY 301 AAATCATCATCGACAGAGAGCAAGATACATGAATGGGAGATTTCCAAATGACGCGC 360
DB 344 AAATCATCATCGACAGAGAGCAAGATACATGAATGGGAGATTTCCAAATGACGCGC 403
QY 361 AGATCTGCGCAGAGAGCGCAGAGTCTGTAATGATTCATATGCGAAGCAATTAATGCA 420
DB 404 AGATCTGCGCAGAGAGCGCAGAGTCTGTAATGATTCATATGCGAAGCAATTAATGCA 463
QY 421 GGTTCGTCATATCTGCTTAGCGTTCTAAAGGAGAACCAACCAAAAGATTTTGTATTA 480
DB 464 AGTTCGTCATATCTGCTTAGCGTTCTAAAGGAGAACCAACCAAAAGATTTTGTATTA 523
QY 481 CAATATCATATATCCGCTCTAATCTGAAGCAATTAATGCGAAGGCTCCGGAACCGTGG 540
DB 524 CAATATCATATATCCGCTCTAATCTGAAGCAATTAATGCGAAGGCTCCGGAACCGTGG 583
QY 541 GTTCCTCATATTAAGTCTCTTTCTTCTAATACGTTCTGACGAGATGACGAATGGCGC 600

DB 584 GTTCCTCATATTAAGTCTCTTTCTTTCATCAATGCTTCTTAACGAATGACGAATGGCGC 643
QY 601 GATTAATTAATTTGCGGAGCGGTGACGCTGCGCGCCCGGATAGACCTGTAATCATCTGC 660
DB 644 GATTAATTAATTTGCGGAGCGGTGACGCTGCGCGCCCGGATAGACCTGTAATCATCTGC 703
QY 661 GAGGTGATTCAGAAACAGGAGAGAGCATGATGGGCGGTGCGTAAAGGCCACATTAATAT 720
DB 704 GAGGTGATTCAGAAACAGGAGAGAGCATGATGGGCGGTGCGTAAAGGCCACATTAATAT 763
QY 721 CTCAGTGAACCTAGACCTTCAATGTCGAGTCTTCGATGATGTCAGTAATACGTC 780
DB 764 CTCAGTGAACCTAGACCTTCAATGTCGAGTCTTCGATGATGTCAGTAATACGTC 823
QY 781 ATTGATGACATCGACCGCATTAATCTTAAGCTTAAGACCTGGAAGAAATTCCTGGGCGC 840
DB 824 ATTGATGACATCGACCGCATTAATCTTAAGCTTAAGACCTGGAAGAAATTCCTGGGCGC 883
QY 841 CAGAAAGATTGGCAATCAAAATTCGAAAGTACGTAAGCGCAAGTCAAAATTAAGCGCAATC 900
DB 884 CAGAAAGATTGGCAATCAAAATTCGAAAGTACGTAAGCGCAAGTCAAAATTAAGCGCAATC 943
QY 901 CCAGCAATCGTGTCTTTCATCTCTGTCGAGGTGCGACGATTAAGAGTTCCTTACAA 960
DB 944 CCAGCAATCGTGTCTTTCATCTCTGTCGAGGTGCGACGATTAAGAGTTCCTTACAA 1003
QY 961 GCGAAATTCAGAGTCTCAAGAACTGAGCTATCAAGATTCGATCTTCATCACCCTCACA 1020
DB 1004 GCGAAATTCAGAGTCTCAAGAACTGAGCTATCAAGATTCGATCTTCATCACCCTCACA 1063
QY 1021 GCCCCCCCTATCAAGAGACACACAGGAGCAAGAAACGGGCAATCGAAGGCGCAG 1080
DB 1064 GCCCCCCCTATCAAGAGACACACAGGAGCAAGAAACGGGCAATCGAAGGCGCAG 1123
QY 1081 GGT 1083
DB 1124 GGT 1126

RESULT 2
US-08-838-151A-5
; Sequence 5, Application US/08838151A
; Publication No. US20010011379A1
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminiviruses
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Dresler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260

```

TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle Gemini Virus
STRAIN: Florida
FEATURE:
NAME/KEY: CDS
LOCATION: 44..1127
US-08-838-151A-5

Query Match      96.5%; Score 1044.6; DB 8; Length 1169;
Best Local Similarity 97.8%; Pred. No. 2,4e-312;
Matches 1059; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

QY 1 ATGCCCCCAGCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTACTTATCCAG 60
DB 44 ATGCCCCCAGCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTACTTATCCAG 103
QY 61 TGGCTCTATCTAAAGAAAGACCTTCCCAATTACAAACCTAAATACCCAGTCAAC 120
DB 104 TGGCTCTATCTAAAGAAAGACCTTCCCAATTACAAACCTAAATACCCAGTCAAC 163
QY 121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAATGGGGAACCTCATCTTCATGTG 180
DB 164 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAATGGGGAACCTCATCTTCATGTG 223
QY 181 CTGTTTCAGTTCCAGAGTAAGTACCAATGCAAGAAATGAGATTTCTTGACCTGGTCTCC 240
DB 224 CTGTTTCAGTTCCAGAGTAAGTACCAATGCAAGAAATGAGATTTCTTGACCTGGTCTCC 283
QY 241 CCAACCCGCTCAGACATTTCCATCCGATATTCAGGAGCTAAATGAGCTCCGACGTC 300
DB 284 CCAACCCGCTCAGACATTTCCATCCGATATTCAGGAGCTAAATGAGCTCCGACGTC 343
QY 301 AAATCATACATCGACAGAGACGAGATATCATGAGTGGGAGATTTCCAAATCGACGCG 360
DB 344 AAATCATACATCGACAGAGACGAGATATCATGAGTGGGAGATTTCCAAATCGACGCG 403
QY 361 AGATCTGCCAGAGAGGCGCAGCTCTGCTAATGATTCATATGCGAAAGCATTAATGCA 420
DB 404 AGATCTGCCAGAGAGGCGCAGCTCTGCTAATGATTCATATGCGAAAGCATTAATGCA 463
QY 421 GGTTGGGTTCAATCTGCTTAAAGGGGTTCTAAGGGAAGAACCAAAAGATTTTGTATTA 480
DB 464 AGTTGGGTTCAATCTGCTTAAAGGGGTTCTAAGGGAAGAACCAAAAGATTTTGTATTA 523
QY 481 CAAATCATACATCCGCTCTAACTTAAGAAAGATATTTCCAAAGGCTCCGAAACCGTGG 540
DB 524 CAAATCATACATCCGCTCTAACTTAAGAAAGATATTTCCAAAGGCTCCGAAACCGTGG 583
QY 541 GTTCCCTCATTTCAAGTCTCTTTTCACTAAGCTTCTGACGAGATGCGAAATGGGCG 600
DB 584 GTTCCCTCATTTCAAGTCTCTTTTCACTAAGCTTCTGACGAGATGCGAAATGGGCG 643
QY 601 GATATATTTTCGGGACGGGTGACGCTGCGCGCGGATGAGACCTGTAAGTATCATGTC 660
DB 644 GATATATTTTCGGGACGGGTGACGCTGCGCGCGGATGAGACCTGTAAGTATCATGTC 703
QY 661 GAGGGTGATTCAGAAACAGGGAAGACGATGTGGCGGCTGTGGCCCAATTAAT 720
DB 704 GAGGGTGATTCAGAAACAGGGAAGACGATGTGGCGGCTGTGGCCCAATTAAT 763
QY 721 CTCAGTGAACACCTAGACTTCAATGCTGAGTCTTCTGAAATGATGTGCAATTAACGTC 780

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DB 764 CTCAGTGAACACCTAGACTTCAATGCTGAGTCTTCTGAAATGATGTGCAATTAACGTC 823
QY 781 ATTGATGACATCGCACCGCATTTATCTAAAGCTAAAGACATGAAAGATTTGCTGGGCGC 840
DB 824 ATTGATGACATCGCACCGCATTTATCTAAAGCTAAAGACATGAAAGATTTGCTGGGCGC 883
QY 841 CAGAAAGATTGGCAATCAAAATTTGCAAGTAAGTAAAGCCAGTTCAATTAAGGCGGATC 900
DB 884 CAGAAAGATTGGCAATCAAAATTTGCAAGTAAGTAAAGCCAGTTCAATTAAGGCGGATC 943
QY 901 CCAGCAATCGTGTCTTTCAGATCTGCTGAGGCGGCGCAGCTAATAAGTCTTAGACAA 960
DB 944 CCAGCAATCGTGTCTTTCAGATCTGCTGAGGCGGCGCAGCTAATAAGTCTTAGACAA 1003
QY 961 GCAGAAATACAGTCTCAAGAACTGAGTATCAAGATGCGATCTTCATCACTCACA 1020
DB 1004 GCAGAAATACAGTCTCAAGAACTGAGTATCAAGATGCGATCTTCATCACTCACA 1063
QY 1021 GCCCCTCTATCAAGAGACACACAGGACCAAGAAACGGGCAATCAGAAAGCGGCGAG 1080
DB 1064 GCCCCTCTATCAAGAGACACACAGGACCAAGAAACGGGCAATCAGAAAGCGGCGAG 1123
QY 1081 GGT 1083
DB 1124 GGT 1126

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RESULT 3
US-08-838-151A-7
Sequence 7, Application US/08838151A
Publication No. US20010011379A1
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSER: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 1169 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO

```

ORIGINAL SOURCE:
 ORGANISM: Tomato Mottle Gemini Virus
 STRAIN: Florida
 FEATURE:
 NAME/KEY: CDS
 LOCATION: 44..1127
 US-08-838-151A-7

Query Match 96.3%; Score 1043; DB 8; Length 1169;
 Best Local Similarity 97.7%; Pred. No. 7.5e-312;
 Matches 1058; Conservative 0; Mismatches 25; Indels 0; Gaps 0;

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Qy 1 ATGCCCCCACCAGAAATTTAGAGTCACTCAAGAACTATTTCTTCACTTATCCCCAG 60
Db 44 ATGCCCCCACCAGAAATTTAGAGTCACTCAAGAACTATTTCTTCACTTATCCCCAG 103
Qy 61 TGTCTCTATCTAAAGAAAGACCTTTCCCAATTACAAAACCTAAATACCCAGTCAAC 120
Db 104 TGTCTCTATCTAAAGAAAGACCTTTCCCAATTACAAAACCTAAATACCCAGTCAAT 163
Qy 121 AAGAAATTCCTCAAAATTTGACAGAGCTTCATGAAATGCGGAACTCTCATCTCCATGTG 180
Db 164 AAGAAATTCCTCAAAATTTGACAGAGCTTCATGAAATGCGGAACTCTCATCTCCATGTG 223
Qy 181 CTGTTCAGTTCGAGAGTGAATGCAATGCAAGATTAACAGATTCCTGCACTGTCTCC 240
Db 224 CTGTTCAGTTCGAGAGAGTGAATGCAATGCAAGATTAACAGATTCCTGCACTGTCTCC 283
Qy 241 CCAACCCGCTGACGACATTTCCATCCGAAATATTCAGGAGCTAAATGAGCTCCGACGTC 300
Db 284 CCAACCCGCTGACGACATTTCCATCCGAAATATTCAGGAGCTAAATGAGCTCCGACGTC 343
Qy 301 AAATCATACATCCGACAGAGCGAGATACATGGAATGGGAGATTCCAATGACGAGC 360
Db 344 AAATCATACATCCGACAGAGCGAGATACATGGAATGGGAGATTCCAATGACGAGC 403
Qy 361 AGATCTGCGCAGAGAGGCGCAGAGTCTGTAATGATTCATATGCGAAAGATTAATGCA 420
Db 404 AGATCTGCGCAGAGAGGCGCAGAGTCTGTAATGATTCATATGCGAAAGATTAATGCA 463
Qy 421 GGTTCGCTCAATTCGCTTAAAGCGGTTCTAAAGGAAACAACCAAAAGATTTGTATTA 480
Db 464 AGTTCGCTCAATTCGCTTAAAGCGGTTCTAAAGGAAACAACCAAAAGATTTGTATTA 523
Qy 481 CAAATCATACATCCGCTCAACCTAAGCAATATTCGAAAGGCTCCGGAACCGTGG 540
Db 524 CAAATCATACATCCGCTCAACCTAAGCAATATTCGAAAGGCTCCGGAACCGTGG 583
Qy 541 GTTCCTTCATTTCAAGTCTCTTTCTTCACTAAACGTTCTCTGACGAGATGAGGAGC 600
Db 584 GTTCCTTCATTTCAAGTCTCTTTCTTCACTAAACGTTCTCTGACGAGATGAGGAGC 643
Qy 601 GATTAATTTATTCGGGACGGGTGACGCTGCGCGCCGGAATGACCTGTAAGTATCATGTC 660
Db 644 GATTAATTTATTCGGGACGGGTGACGCTGCGCGCCGGAATGACCTGTAAGTATCATGTC 703
Qy 661 GAGGAGTATTCAGAAACAGGGAAGACGATGCGGCGGTTAGGCCCCAATAATAT 720
Db 704 GAGGAGTATTCAGAAACAGGGAAGACGATGCGGCGGTTAGGCCCCAATAATAT 763
Qy 721 CTCAGTGAACCTAGACTTCATGATGTCAGTCTTCTCGATGATGTCAGTATTAACGTC 780
Db 764 CTCAGTGAACCTAGACTTCATGATGTCAGTCTTCTCGATGATGTCAGTATTAACGTC 823
Qy 781 ATTGATGACATTCGACCGCATTTATCTAAAGCTAAAGACTGGAAGAAATGCTGGGGCC 840
Db 824 ATTGATGACATTCGACCGCATTTATCTAAAGCTAAAGACTGGAAGAAATGCTGGGGCC 883
Qy 841 CAGAAAGATTTGGAAGTGAATTTGCAAGTGAAGGCAAGTCAATTAAGGCGGAAATC 900
Db 884 CAGAAAGATTTGGAAGTGAATTTGCAAGTGAAGGCAAGTCAATTAAGGCGGAAATC 943
Qy 901 CAGCAATCGTGTTCGAAATCTGTGTAGGAGTGCAGCTAATAAGAGTTCTTAGACAAA 960
  
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Db 944 CAGCAATCGTGTTCGAAATCTGTGTAGGAGTGCAGCTAATAAGAGTTCTTAGACAAA 1003
Qy 961 GCAGAAATACAGGCTCTCAAGAACTGAGACTATCAAGAAATGCACTTTCATCACCTCACA 1020
Db 1004 GCAGAAATACAGGCTCTCAAGAACTGAGACTATCAAGAAATGCACTTTCATCACCTCACA 1063
Qy 1021 GCCCCCCCTTATCAAGAGACACACAGGCAAGCCAAAGAAACGGGCAATCAGAAAGCGCAG 1080
Db 1064 GCCCCCCCTTATCAAGAGACACACAGGCAAGCCAAAGAAACGGGCAATCAGAAAGCGCAG 1123
Qy 1081 GGT 1083
Db 1124 GGT 1126
  
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RESULT 4
US-08-838-151A-17/c
Sequence 17, Application US/08838151A
Publication No. US20010011379A1
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSER: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 2602 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Tomato Mottle GeminiVirus
STRAIN: Florida
US-08-838-151A-17
  
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Query Match 96.1%; Score 1040.8; DB 8; Length 2602;
 Best Local Similarity 98.0%; Pred. No. 5.5e-311;
 Matches 1054; Conservative 0; Mismatches 22; Indels 0; Gaps 0;

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Qy 8 CACCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTCACTTATCCCCAGTGTCTC 67
Db 2602 CACCAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTCACTTATCCCCAGTGTCTC 2543
  
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QY 68 TATCTAAGAGAGACGCTTCCCAATTACAAAACCTAAATACCCTGTCACAGAAAT 127
DB 2542 TGCTAAGAGAGAGACGCTTCCCAATTACAAAACCTAAATACCCTGTCACAGAAAT 2483
QY 128 TCATCAAAATTTGACAGAGCTTCAATGAAATGGGGAACCTCATCTCCATGCTGTTTC 187
DB 2482 TCATCAAAATTTGACAGAGCTTCAATGAAATGGGGAACCTCATCTCCATGCTGTTTC 2423
QY 188 AGTTGAGAGTAAAGTACCAATGACAGATTAACAGATTCTTGAAGCTGCTCCCAACC 247
DB 2422 AGTTGAGAGTAAAGTACCAATGACAGATTAACAGATTCTTGAAGCTGCTCCCAACC 2263
QY 248 GGTGAGACATTTCCATCCGAAATTTTACGAGAGCTAAATGAGCTCCGACGTAATCAT 307
DB 2362 GGTGAGACATTTCCATCCGAAATTTTACGAGAGCTAAATGAGCTCCGACGTAATCAT 2303
QY 308 ACATCGACAAAGACGAGATACATGGAATGGGGAGATTTCCAAATGACAGGAGATCTG 367
DB 2302 ACATCGACAAAGACGAGATACATGGAATGGGGAGATTTCCAAATGACAGGAGATCTG 2243
QY 368 CCAGAGAGGCGCAGAGCTGCTAATGATTCATATGCGAAAGATTAATGACAGTTCCG 427
DB 2242 CCAGAGAGGCGCAGAGCTGCTAATGATTCATATGCGAAAGATTAATGACAGTTCCG 2183
QY 428 TTCAATCTGCTTACGCGTTCTTAAGGGAAGACACCAAAAGATTTGTATTAACAAATC 487
DB 2182 TTCAATCTGCTTACGCGTTCTTAAGGGAAGACACCAAAAGATTTGTATTAACAAATC 2123
QY 488 ATAAACATCGGCTTAACTCTAAGACGAATATTCGAAAGGCTCCGGAACGCTGGGTTCTC 547
DB 2122 ATAAACATCGGCTTAACTCTAAGACGAATATTCGAAAGGCTCCGGAACGCTGGGTTCTC 2063
QY 548 CATTTAAGTCTCTTCTTCTAATGATTCGAGATGACAGATGAGGAGCTGATTAAT 607
DB 2062 CATTTAAGTCTCTTCTTCTAATGATTCGAGATGACAGATGAGGAGCTGATTAAT 2003
QY 608 ATTTGCGGAGCGGTGACGCTGCGCCCGGATAGACTGTAATGATATGATGAGGCTG 667
DB 2002 ATTTGCGGAGCGGTGACGCTGCGCCCGGATAGACTGTAATGATATGATGAGGCTG 1943
QY 668 ATTCAAGAACAGGGAAGACGATGAGGCGGCTGTTAGGCGCAATTAATCTCATG 727
DB 1942 ATTCAAGAACAGGGAAGACGATGAGGCGGCTGTTAGGCGCAATTAATCTCATG 1883
QY 728 GACACCTAGACTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 787
DB 1882 GACACCTAGACTTCAATGATGATGATGATGATGATGATGATGATGATGATGATG 1823
QY 788 ACATCGCAGCGCATTTATTAAGCTAAGACATGGAAGATGCTGGGGCCCAAG 847
DB 1822 ACATCGCAGCGCATTTATTAAGCTAAGACATGGAAGATGCTGGGGCCCAAG 1763
QY 848 ATTGGCAATCAATTTGCAATGAGGTGAGGAGGATGATTAAGGCGGAATCCAGCAA 907
DB 1762 ATTGGCAATCAATTTGCAATGAGGTGAGGAGGATGATTAAGGCGGAATCCAGCAA 1703
QY 908 TCGTGTCTTTCGAATCTGCTGAGGCTGACGATTAAGAGTTCTTGAACAAAGCAGAAA 967
DB 1702 TCGTGTCTTTCGAATCTGCTGAGGCTGACGATTAAGAGTTCTTGAACAAAGCAGAAA 1643
QY 968 ATACAGGCTCAAGAACTGACATATCAAGATGCGATCTTCATCACTCAAGCCCCC 1027
DB 1642 ATACAGGCTCAAGAACTGACATATCAAGATGCGATCTTCATCACTCAAGCCCCC 1583
QY 1028 TCATCAAGAGACACACAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1083
DB 1582 TCATCAAGAGACACACAGAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 1527

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RESULT 5
 US-08-838-151A-3
 ; Sequence 3, Application US/08838151A
 ; Publication No. US20010011379A1

```

? GENERAL INFORMATION:
? APPLICANT: Stout, John T
? APPLICANT: Lau, Hang T
? APPLICANT: Maxwell, Douglas
? APPLICANT: Ahlquist, Paul
? APPLICANT: Hanson, Steve
? TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
? TITLE OF INVENTION: Genes
? NUMBER OF SEQUENCES: 63
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Dressler, Rocky, Milnamow & Katz
? STREET: Two Prudential Plaza, Suite 4700
? CITY: Chicago
? STATE: Illinois
? COUNTRY: U.S.A.
? ZIP: 60601
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patent Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SVS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 3:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 1169 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: circular
? MOLECULE TYPE: DNA (genomic)
? HYPOTHEICAL: NO
? ANTI-SENSE: NO
? ORIGINAL SOURCE:
? ORGANISM: Tomato Mottle Gemini Virus
? STRAIN: Florida
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 44..1127
? PUBLICATION INFORMATION:
? AUTHORS: Gilbertson, RL et al.
? TITLE: Pseudorecombination between the infectious
? TITLE: cloned DNA components of tomato mottle and bean
? TITLE: dwarf mosaic geminivirus.
? JOURNAL: Journal of General Virology
? VOLUME: 74
? PAGES: 23-31
? DATE: 1993
?
? US-08-838-151A-3
?
? Query Match 96.0%; Score 1039.8; DB 8; Length 1169;
? Best Local Similarity 97.5%; Pred. No. 7.3e-111;
? Matches 1056; Conservative 0; Mismatches 27; Indels 0; Gaps 0;

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QY 1 ATGCCCCCAACCAAGAAATTTAGATTCAATCAAGAACTATTTCTTAATCCCAAG 60
DB 44 ATGCCCCCAACCAAGAAATTTAGATTCAATCAAGAACTATTTCTTAATCCCAAG 103
QY 61 TGCTCTCTATCTAAGAAAGACATTTCCCAATTAACAAACCTAAATCCCAAGCAAC 120
DB 104 TGCTCTCTCTAAGAAAGACATTTCCCAATTAACAAACCTAAATCCCAAGCAAT 163
QY 121 AAGAAATTCATCAAAATTTGACAGAGCTTCAATGAAGATGGGGAACCTATCTCATGTG 180
DB 164 AAGAAATTCATCAAAATTTGACAGAGCTTCAATGAAGATGGGGAACCTATCTCATGTG 223

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QY 181 CTTGTCAGTTCGAGGTAAGTACCAATGACAGATAACAGATTCTTCCAGCTGCTCC 240
 Db 224 CTTGTCAGTTCGAGGTAAGTACCAATGACAGATAACAGATTCTTCCAGCTGCTCC 283
 QY 241 CCAACCCGGTCAGACATTTTCATCCGAATATTCAGGAGCTAATTCAGCTCCGAGTC 300
 Db 284 CCAACCCGGTCAGACATTTTCATCCGAATATTCAGGAGCTAATTCAGCTCCGAGTC 343
 QY 301 AATCATATCATCGACAGACGAGATACATTCGATGGGAGATTTTCCAAATGACGGC 360
 Db 344 AATCATATCATCGACAGACGAGATACATTCGATGGGAGATTTTCCAAATGACGGC 403
 QY 361 AGATCTGCGAGAGGCGACGAGCTGCTAATGATTCATATGCGAAGCATTAATGCA 420
 Db 404 AGATCTGCGAGAGGCGACGAGCTGCTAATGATTCATATGCGAAGCATTAATGCA 463
 QY 421 GATTGCGTCAATCTGCTTACGCGTTCCTAAGGAGAACCAACCAAAAGATTTGTATTA 480
 Db 464 AGTTGCGTCAATCTGCTTACGCGTTCCTAAGGAGAACCAACCAAAAGATTTGTATTA 523
 QY 481 CAAATATATATCCGCTCTTACCTTGAACGAATATTCGCAAGGCTCCGGAACCGTGG 540
 Db 524 CAAATATATATCCGCTCTTACCTTGAACGAATATTCGCAAGGCTCCGGAACCGTGG 583
 QY 541 GTTCCTCATTTCAAGTCTCTTTCACTAAGCTTCTGACGAGATGACGAATGGGCG 600
 Db 584 GTTCCTCATTTCAAGTCTCTTTCACTAAGCTTCTGACGAGATGACGAATGGGCG 643
 QY 601 GATATATATTTCCGAGCGGTGACGCTGCGCGCGGATGACCTGTATGATCATGTC 660
 Db 644 GATATATATTTCCGAGCGGTGACGCTGCGCGCGGATGACCTGTATGATCATGTC 703
 QY 661 GAGGTGATTCAGAGACAGGAGAACGATGGGCGGCTGCTTAAGCCCATTAATCAT 720
 Db 704 GAGGTGATTCAGAGACAGGAGAACGATGGGCGGCTGCTTAAGCCCATTAATCAT 763
 QY 721 CTCAGTGAACCTGAGACTTCAATGATGAGTCTTCTCGAATGATGTCAGTATTAAGTC 780
 Db 764 CTCAGTGAACCTGAGACTTCAATGATGAGTCTTCTCGAATGATGTCAGTATTAAGTC 823
 QY 781 ATTGATGATCATCGACCGCATTTATCTAAGCTAAGACCTGGAAGAAATGCTGGGGCC 840
 Db 824 ATTGATGATCATCGACCGCATTTATCTAAGCTAAGACCTGGAAGAAATGCTGGGGCC 883
 QY 841 CAGAAATATGCGAATTAATGCAATGCGTAAAGCAAGTTCATTAATTAAGGCGAATC 900
 Db 884 CAGAAATATGCGAATTAATGCAATGCGTAAAGCAAGTTCATTAATTAAGGCGAATC 943
 QY 901 CCAAGCATCGTCTTTCGAATCTGATGAGGTCGCGACTAATAAGATTCTTAGACAAA 960
 Db 944 CCAAGCATCGTCTTTCGAATCTGATGAGGTCGCGACTAATAAGATTCTTAGACAAA 1003
 QY 961 GCAAAATATCAGGTCTCAAGAACTGATCTATCAAGATGCGATCTTCAATCAACCTCA 1020
 Db 1004 GCAAAATATCAGGTCTCAAGAACTGATCTATCAAGATGCGATCTTCAATCAACCTCA 1063
 QY 1021 GCCCCCCCTATCAAGAGACACAGGCAAGCCAAAGACCGGCAATCGAAGGCGCAG 1080
 Db 1064 GCCCCCCCTATCAAGAGACACAGGCAAGCCAAAGACCGGCAATCGAAGGCGCAG 1123
 QY 1081 GGT 1083
 Db 1124 GGT 1126

RESULT 6

US-08-838-151A-13

; Sequence 13, Application US/08838151A

; Publication No. US20010011379A1

; GENERAL INFORMATION:

; APPLICANT: Stout, John T

; APPLICANT: Luu, Hang T

; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESS: Dressler, Rocky, Milamow & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.
 ; ZIP: 60601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/838,151A
 ; FILING DATE:
 ; CLASSIFICATION: 800
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mueller, Lisa V
 ; REGISTRATION NUMBER: 38,978
 ; REFERENCE/DOCKET NUMBER: SVS3801P0260
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-616-5400
 ; TELEFAX: 312-616-5460
 ; INFORMATION FOR SEQ ID NO: 13:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 1166 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: DNA (genomic)
 ; HYPOTHEICAL: NO
 ; ANTI-SENSE: NO
 ; ORIGINAL SOURCE:
 ; ORGANISM: Tomato Mottle GeminiVirus
 ; INDIVIDUAL ISOLATE: Florida
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: 44..436
 ; US-08-838-151A-13
 Query Match 95.5%; Score 1033.8; DB 8; Length 1166;
 Best Local Similarity 97.6%; Pred. No. 5.3e-309;
 Matches 1061; Conservative 0; Mismatches 22; Indels 4; Gaps 1;

QY	361	A-----GATCTCCAGAGGAGCCAGCAGCTCTGCTAATATTCATATGCGAAGCACTTAA	416
Db	404	AGATCGATCTGCCAGAGGAGCCAGCAGCTCTGCTAATATTCATATGCGAAGCACTTAA	463
QY	417	TGCAGTTCCGTTCAATCTGCTTACGCGTTCTAAAGGAGAACAACCAAAAGATTGGT	476
Db	464	TGCAAGTTCCGTTCAATCTGCTTACGCGTTCTAAAGGAGAACAACCAAAAGATTGGT	523
QY	477	ATTTCAAAATCATTAACATCCGCTCTAACCTTGAAACGAATATTTCGAAAGGCTCGGAAC	536
Db	524	ATTTCAAAATCATTAACATCCGCTCTAACCTTGAAACGAATATTTCGAAAGGCTCGGAAC	583
QY	537	GTGGGTTCCCTCATTTCAAGTCTCTTCTTCACTAACGTTCTGTGCGAGATGACAGATG	596
Db	584	GTGGGTTCCCTCATTTCAAGTCTCTTCTTCACTAACGTTCTGTGCGAGATGACAGATG	643
QY	597	GCGCGATTAATTATTTCCGGAACCGGTGACGCTGCGCGCCGATAGACCTGTAAAGTATCAT	656
Db	644	GCGCGATTAATTATTTCCGGAACCGGTGACGCTGCGCGCCGATAGACCTGTAAAGTATCAT	703
QY	657	CGTGCAGGGGTATTTCAAGAACAGGGAGAACAAGATGTGGCGCGTGCCTTAAGGCCACATAA	716
Db	704	CGTGCAGGGGTATTTCAAGAACAGGGAGAACAAGATGTGGCGCGTGCCTTAAGGCCACATAA	763
QY	717	CTATCTCAGTGGAGACCTGAGACTTCAATGTCGAGTCTTCTCGAATGATGTGCAATATA	776
Db	764	CTATCTCAGTGGAGACCTGAGACTTCAATGTCGAGTCTTCTCGAATGATGTGCAATATA	823
QY	777	CGTCATTGATGACATCGCACCGCATTAATCTAAAGCTTAAAGCACTGGAAGAAGATTGCTGGG	836
Db	824	CGTCATTGATGACATCGCACCGCATTAATCTAAAGCTTAAAGCACTGGAAGAAGATTGCTGGG	883
QY	837	GGCCCGAAGAAATTGGCAATCAAAATTGCAAGTACGGTAAAGCCAGTTCAAATTTAAAGCGG	896
Db	884	GGCCCGAAGAAATTGGCAATCAAAATTGCAAGTACGGTAAAGCCAGTTCAAATTTAAAGCGG	943
QY	897	AATCCCAAGCAATCGTGCTTGGCAATCCCGTGTGAAGGTCACGACTATAAGAGTTCTTGA	956
Db	944	AATCCCAAGCAATCGTGCTTGGCAATCCCGTGTGAAGGTCACGACTATAAGAGTTCTTGA	1003
QY	957	CAAGACGAATAATACAGGTCTCAAGAACTGGAAGTTCAGAGATGCGATCTTCATCACCCCT	1018
Db	1004	CAAGACGAATAATACAGGTCTTAAAGACTGGAAGTTCAGAGATGCGATCTTCATCACCCCT	1065
QY	1017	CACAGCCCCCTCTATCAAGAGACACACAGGCAAGCCAAAGAAACGGGCAATCAGAAAGGC	1078
Db	1064	CACAGCCCCCTCTATCAAGAGACACACAGGCAAGCCAAAGAAACGGGCAATCAGAAAGGC	1125
QY	1077	GCAGGGT 1083	
Db	1124	GCAGGGT 1130	

RESULT 7
 US-08-838-151A-15
 ; Sequence 15, Application US/08838151A
 ; Publication No. US20010011379A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Scout, John T
 ; APPLICANT: Lau, Hang T
 ; APPLICANT: Maxwell, Douglas
 ; APPLICANT: Ahlquist, Paul
 ; APPLICANT: Hanson, Steve
 ; TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
 ; TITLE OF INVENTION: Genes
 ; NUMBER OF SEQUENCES: 63
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
 ; STREET: Two Prudential Plaza, Suite 4700
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: U.S.A.

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1 ZIP: 60601
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3 COMPUTER READABLE FORM:
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5 MEDIUM TYPE: Floppy disk
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7 COMPUTER: IBM PC compatible
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9 OPERATING SYSTEM: PC-DOS/MS-DOS
10
11 SOFTWARE: Patentn Release #1.0, Version #1.30
12
13 CURRENT APPLICATION DATA:
14
15 APPLICATION NUMBER: US/08/838,151A
16
17 FILING DATE:
18
19 CLASSIFICATION: 800
20
21 ATTORNEY/AGENT INFORMATION:
22
23 NAME: Mueller, Lisa V
24
25 REGISTRATION NUMBER: 38,978
26
27 REFERENCE/DOCKET NUMBER: SYS901P0260
28
29 TELECOMMUNICATION INFORMATION:
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31 TELEPHONE: 312-616-5400
32
33 TELEFAX: 312-616-5460
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35 INFORMATION FOR SEQ ID NO: 15:
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37 SEQUENCE CHARACTERISTICS:
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39 LENGTH: 1246 base pairs
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41 TYPE: nucleic acid
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43 STRANDEDNESS: single
44
45 TOPOLOGY: circular
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47 MOLECULE TYPE: DNA (genomic)
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49 HYPOTHEITICAL: NO
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51 ANTI-SENSE: NO
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53 ORIGINAL SOURCE:
54
55 ORGANISM: Tomato Mottle Geminivirus
56
57 STRAIN: Florida
58
59 PUBLICATION INFORMATION:
60
61 AUTHORS: Gilbertson, RL
62
63 AUTHORS: Hidayat, SH
64
65 AUTHORS: Papiolatas, EJ
66
67 AUTHORS: Rojas, MR
68
69 AUTHORS: Hou, YM
70
71 AUTHORS: Maxwell, DP
72
73 TITLE: Pseudorecombination between the infectious
74
75 TITLE: cloned DNA components of tomato mottle and bean
76
77 TITLE: dwarf mosaic geminiviruses.
78
79 JOURNAL: Journal of General Virology
80
81 VOLUME: 74
82
83 PAGES: 23-31
84
85 DATE: 1993
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90 US-08-838-151A-15
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Db 601 GACGACTATTCCGAGAGGGGTTCCGCTCCGCGCGCGGAGAAAGCCTATTAGTATCATCTC 660
Qy 661 GAGGTGATTTCAAGAACAGGAGAGACGATGTGGCGCGTCTAGGCCACATTAATAT 720
Db 661 GAGGTGATTTCAAGAACAGGAGAGACATGTGGCGTCTAGGCCACATTAATAT 720
Qy 721 CTGAGTGACACTAGACTTCAATTCGATGTGAGTCTTTCGATATGTGACATTAACGTC 780
Db 721 TTGAGCGGTCTATTGGACCTTAATTCACGTGTCTATTCCACGAGTGGAAATCAACGTC 780
Qy 781 ATTGATGACATCGACCGCATTTATCTTAAGCTAAAGCAGGAAAGATGTGGGGGCC 840
Db 781 ATTGATGACATTAAGCCCAATTTATTTGAATTAAGCAGTGAAGAACTAATTTGGGCA 840
Qy 841 CAGAAAGATTGGCAATCAATTAATTCAGTACGTAAGCCAGTTCGAATTAAGCGGATC 900
Db 841 CAAAGGACTGGCAATCTAATCTGAATTAATGAAGCGGTTCAATTAAGAGGAAATA 900
Qy 901 CCAGCAATCGTCTTTGCAATCTCTGTGAGGGTCCAGCTATAAGAGTTCTTAGACAA 960
Db 901 CCATCAATCGTCTTTGCAATCTCAAGTGAAGGTTCCAGTTATAAGACTTCTGACAAA 960
Qy 961 GCAGAAATACAGGTCTCAAGAACTGACTATCAAGAAAGATCTTCAATCACCTGACA 1020
Db 961 GAAAGAAACCGAGCTTTACCAACTGACTATTTCAATATGAGATCTTCTGACCTTACA 1020
Qy 1021 GCCCCTCTATCAAGAGACACACAGGCAAGCCCAAGAAACGGGCAATCAGAAAGCG 1077
Db 1021 GCCCCTCTATCAAGAGACACACAGGATTTGCCAAACGTAAGCCATTTGTGAGG 1077

RESULT 9
US-08-838-151A-45
; Sequence 45, Application US/08838151A
; Publication No. US20010011379A1
GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 45:
SEQUENCE CHARACTERISTICS:
LENGTH: 1183 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bean Golden Mosaic Geminiivirus
; STRAIN: Type II
; INDIVIDUAL ISOLATE: Guatemala
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1059
US-08-838-151A-45
Query Match 64.1%; Score 694.6; DB 8; Length 1183;
Best Local Similarity 77.8%; Pred.No.6.2e-204;
Matches 838; Conservative 0; Mismatches 239; Indels 0; Gaps 0;
Qy 1 ATGCCCCCAACAAAGAAATTTAGTTCAGTCAAAAGACTATTTCTTAATTCACAG 60
Db 1 ATGCAACACCTCAAGATTTAGAGTTCAAGTCAAAAGACTATTTCTTAATTCACAG 60
Qy 61 TGCTCTATCTAAGAGAGACACTTTCCAATTACAAAACCTAATACCCAGTCAAC 120
Db 61 TGCCCTATACCAAGAGAGAGTCTTTCGCACTTCAAGAGATTCAGCAGCAAT 120
Qy 121 AAGAAATTCACAAATTTGCAAGAGCTTCATGAATAATGGGAACTCATCTCATGTG 180
Db 121 AAAAAATTCATCAAGAGTCTGAGAGACGTCAAGAAATGATGAACTCATCTCATGTG 180
Qy 181 CTGTTCAGTTCGAAGATTAAGTCAATGACAGATTAAGATTTCTTCGACTGTCTCC 240
Db 181 CTATTCATTCGAAGATTAATTCGTCTGACAAATTAAGATTTCTTCGACTGTCTCC 240
Qy 241 CCAACCCGTCAGACATTTCCATCCGAATTTCAAGGAGCTTAATCGAGCTCCAG 300
Db 241 TCAACGAGTCAGACCTTTCCATCCGAACATTCAGGAGCTTAATCAAGTTCAGAG 300
Qy 301 AATCATCATTCAGACAGAGAGAGATTAATGATGATGGGAGATTTCCAAATCGAG 360
Db 301 AAGCAATCATTCAGACAGAGAGATTAATGATGATGGGAGATTTCCAAATCGAG 360
Qy 361 AGATTCGCGAGAGAGAGAGAGAGTGTGCTGAATGATTCATGCGAAGCATTAATGCA 420
Db 361 AGATTCGCGAGAGAGAGAGAGAGTGTGCTGAATGATTCATGCGAAGCATTAATGCA 420
Qy 421 GGTTCGCTCAATCTCTTACGCGTCTTAAGGAGAAACAACAAAGATTTGTATTA 480
Db 421 GATTCATTAATCTCTCTTGAATTAATGAAGAGAAACAACAAAGATTTGTATTA 480
Qy 481 CAAATCATTAATCTCTCTTGAATTAATGAAGAGATTTGTGAAGAGCTCCGAAAC 540
Db 481 CAACATCAATCTCTCTTGAATTAATGAAGAGATTTGTGAAGAGCTCCGAAAC 540
Qy 541 GTTCTCAATTTCAAGTCTCTTCACTTAAGTTCGACAGATTCAGAGATTCAGAG 600
Db 541 GTTCTCAATTTCTGTTGATCATTCGCAATGTTCCGTTTATGCAAGATGGGTT 600
Qy 601 GATTAATTTTTCGGAACGGGTGAACGCTGCGCCGCGAGATAGACTTAATCATCTG 660
Db 601 GACGACTATTTCGGAAGGGGTTCCGCTGCGCGCCGGAAGACTTAATGATCATCTG 660
Qy 661 GAGGTGATTTCAAGAACAGGAGAGACATGTGGCGCGTCTAGGCCACATTAAT 720
Db 661 GAGGTGATTTCAAGAACAGGAGAGACATGTGGCGCGTCTAGGCCACATTAAT 720
Qy 721 CTGAGTGACACTAGACTTCAATTCGATGTGAGTCTTTCGATATGTGACATTAACG 780
Db 721 TTGAGCGGTCTATTGGACCTTAATTCACGTGTCTATTCCACGAGTGGAAATCAAC 780
Qy 781 ATTGATGACATCGACCGCATTTATCTTAAGCTAAAGCAGTGAAGAACTAATTTGG 840
Db 781 ATTGATGACATTAAGCCCAATTTATTTGAATTAAGCAGTGAAGAACTAATTTGG 840
Qy 841 CAGAAAGATTGGCAATCAATTCGAAGTACGGAAGCCAGTTCAAATTAAGCGGAATC 900

Db 841 CAAAGAGCTGGCATCTAATCTAATATGGAAGACCGGCTTCAATTAAGAGGAATA 900
Qy 901 CCAGCAATCGTGTCTTTGCAATCTGTGAGGGTCCAGCTAATAAGAGTTCTTAGACAAA 960
Db 901 CCATCAATCGTGTGTGCAATCCAGGTGAGGGTTCAGATTATAAGACTTCTCGACAAA 960
Qy 961 GCAGAAATATAGGCTTCAAGACTGACTATCAAGATGCGATCTTCATCACCCTCACA 1020
Db 961 GAAAGAAAACGAGCTTTACACACATGAGCTATTCATATGCGATCTTCGTCACCA 1020
Qy 1021 GCCCCCTCTATCAAGAGACACACAGGCAAGCAACGGGCAATCAGAGGCG 1077
Db 1021 GCCCCCTCTATCAAGACACACAGGATTCGCAACGTAAGCATTGCTGACG 1077

RESULT 10
US-08-838-151A-48
: Sequence 48, Application US/08838151A
: Publication No. US20010011379A1
: GENERAL INFORMATION:
: APPLICANT: Stout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: TITLE OF INVENTION: Genes
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESSES:
: ADDRESSEE: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/838, 151A
: FILING DATE:
: CLASSIFICATION: 800
: ATTORNEY/AGENT INFORMATION:
: NAME: Mueller, Lisa V
: REGISTRATION NUMBER: 38,978
: REFERENCE/DOCKET NUMBER: SVS3801P0260
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-616-5400
: TELEFAX: 312-616-5460
: INFORMATION FOR SEQ ID NO: 48:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1062 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: MOLECULE TYPE: circular
: TOPOLOGY: circular
: HYPOTHETICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Bean Golden Mosaic Geminivirus
: STRAIN: Type II
: INDIVIDUAL ISOLATE: Guatemala
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 1..1059
US-08-838-151A-48

Query Match 63.8%; Score 691.2; DB 8; Length 1062;
Best Local Similarity 78.4%; Pred. No. 6.6e-203;
Matches 828; Conservative 0; Mismatches 228; Indels 0; Gaps 0;

Qy 1 ATGCCCCACCAAGAAATTTAGATTGATCAAGAACTATTCTTAATATCCCCAG 60
Db 1 ATGCCACACCTCAAGATTTAGATTGATCAAGAACTATTCTTAATATCCCTGT 60
Qy 61 TGCTCTATCTAAGAAAGAACCTTCCCAATTACAAAACCTAAATACCCAGTCAAC 120
Db 61 TGCCCTATACGAAAGAAAGAAATTTCTTGCAACTTCAGAAAGATTCAAGCCAGCAAT 120
Qy 121 AAGAAATTCATCAAAATTTGACAGAGCTTCATGAAAATGGGGAACCTCATCTCATGTG 180
Db 121 AAAAATTCATCAAAAGTCTGTGAGAACGTCAGAGATGCTGAACCTCATCTTCAGTGG 180
Qy 181 CTGTGAGTTGCAAGGTAAGTACCAATGACGAAATACAGATTCTTCGACTGCTCC 240
Db 181 CTATTTCAATTCGAGGTAATTTGTCGACAAATTAAGATTTGTCGACTGCTATCC 240
Qy 241 CCAACCCGATCAGACATTTTCATCCGAATATTCAAGGACTTAATGAGCTCCGACGTC 300
Db 241 TCAACGAGTTCAGACACTTTTCATCCGAACTTCAGGAGCTTAATCAAGTTCAGACGTC 300
Qy 301 AAATCATATCATCGACAAAGAGATGAGATACAAATGGAATGGGGAATTTCCAAATCGACGCG 360
Db 301 AAGGCATATCATCGACAAAGATGAGTCAATGGAATGGGGAATTTCCAAATCGACGCG 360
Qy 361 AGATCTCCAGAGAGGCGCAGAGTCTGTAATGATTATATGCGAAGCAATTAATGCA 420
Db 361 AGATCTCCAGAGAGAGGCTGACAGTCTGCCAAGCACTATATGCGAAGCAATTAATGCA 420
Qy 421 GGTTCGGTTCAATCTGCTTAGCGGTTCTAAGGGAAGAACCCAAAGATTTGTAATTA 480
Db 421 GATTCATATGATTCGCTTGAACAATATGAAAGAAAGAACCCGAAGATTAATGCTCTT 480
Qy 481 CAAATCATATATCCGCTCTTAACCTAGAACGAATATTCGCAAAAGGCTCCGGAACCTGG 540
Db 481 CAAATCATATATCCGCTCTTAACCTAGAACGAATATTCGCAAAAGGCTCCGGAACCTGG 540
Qy 541 GTTCCTCATATTCAGAGTCTCTTTCACTAACGTTCTCTGACGAGATGAGAGGCGG 600
Db 541 GTTCCTCATATTCAGAGTCTCTTTCACTAACGTTCTCTGACGAGATGAGAGTGGGTT 600
Qy 601 GATTAATTAATTTGGGAGCGGTTGACGCTGCGCCGCGGATGAGCTGTAAGTATCATGTC 660
Db 601 GACGACTATTTGGGAGCGGTTGACGCTGCGCGCGGCGGAAAGCCTATTAATCATGTC 660
Qy 661 GAGGTATTCAGAAACAGGGAAGACATGTGGGCGGCTGTAGGCCCACTAATAT 720
Db 661 AGAGGTATTCAGAAACAGGGAAGACATGTGGGCGGCTGTAGGCCCACTAATAT 720
Qy 721 CTCAGTGAACCTAGACTTCAATGTGCGAGTCTTCTCGAATGATGTGCAATTAACGTC 780
Db 721 TTGAGCGGTCAATTTGACCTTAATTCACGTGTCTATTCACAGAGTGAATACAGTGC 780
Qy 781 ATTGATGACATCGACCGCATTAATCTAAGCTTAAGCACTGGAAGAAATGCTGGGGCC 840
Db 781 ATTGATGACATTAAGCCCAATTAATTTGAAGTAAAGCACTGGAAGAAATTAATGGGGCA 840
Qy 841 CAGAAATTTGGCAATGAATTTGCAATGAGTAAGCAATGAATTAAGAGGGAATC 900
Db 841 CAAAGGACTGGCAATCTAATCTGAATTAATGGAAGCCGTTCAATTAAGAGGGAATA 900
Qy 901 CCAGCAATCGTGTCTTCAATCTGTGAGGGTCCAGCTAATAAGAGTTCTTAGACAAA 960
Db 901 CCATCAATCGTGTGTGCAATCCAGGTGAGGGTTCAGATTATAAGACTTCTCGACAAA 960
Qy 961 GCAGAAATATAGGCTTCAAGACTGACTATCAAGATGCGATCTTCATCACCCTCACA 1020
Db 961 GAAAGAAAACGAGCTTTACACACATGAGCTATTCATATGCGATCTTCGTCACCACTCACA 1020
Qy 1021 GCCCCCTCTATCAAGAGACACACAGGCAAGCTAA 1056
Db 1021 GCCCCCTCTATCAAGACACACAGGATTCGCA 1056

ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 1062 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bean Golden Mosaic Geminivirus
STRAIN: Type II
INDIVIDUAL ISOLATE: Guatemala
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1059
US-08-838-151A-54

Query Match 63.7%; Score 689.6; DB 8; Length 1062;
Best Local Similarity 78.3%; Pred. No. 2.1e-202;
Matches 827; Conservative 0; Mismatches 229; Indels 0; Gaps 0;

QY 1 ATGCCCCCAACCAAGAAATTAGAGTTCAGTCAAGAACTATTCTTACCTATCCCAAG 60
DB 1 ATGCCCAACCTCAAGATTTAGAGTTCAGTCAAGAACTATTCTTACCTATCTCTGT 60
QY 61 TGCCTCTATCTAAGAAAGAAAGCACTTCCCAATTACAAAACCTAAATACCCCAAGTCAAC 120
DB 61 TGCCTCTATCTAAGAAAGAAAGTCTTTCGCACTTCAGAAAGATTCAATACAGCCAGCAAT 120
QY 121 AAGAAATTCATCAAAATTTGCAAGAGCTTATGAAAATGGGGAACCTCATCTCCATGTG 180
DB 121 AAAAAATTCATCAAAAGTCTGAGAGAACTGACAGAGATGTGAACTCATCTTCATGTG 180
QY 181 CTGTGAGTTCGAAAGTAAAGTACCAATGACAGATTAACAGATTCTTCGACCTGCTGCC 240
DB 181 CTATTATCAATTCGAAAGTAAATTTGCTGCAAAATTAAGATTTGCTGACCTGATATCC 240
QY 241 CCAACCCGCTGAGCAATTCATCCGAATTTTCAGGAGCTAAATCGAGCTCGACGTC 300
DB 241 TCAACCAAGTTCAGCACTTTCATCCGAATTCAGGAGCTAAATCAAGTTCAAGATC 300
QY 301 AAATCATACATCCGACAGAGAGAGATACATCGAATGGGGAGATTTCCAAATGACGGC 360
DB 301 AAGGCAATACATCCGACAAAGATGAGATCAATCGAATGGGGCAATTCAGATGACGGC 360
QY 361 AGATCTCCGAGAGAGGCGAGAGTGTGTAATGATTCAATTTGGGAAGCAATTAATGCA 420
DB 361 AGATCTCCGAGAGAGGCGAGAGTGTGCAACAGATCTATTTGCAAGGCAATTAAGCA 420
QY 421 GGTTCGGTCAATCTGCTTACGCTTCTAAGGAGAACCAACCAAGATTTTGTATTA 480

DB 421 GATTCAATGATATCTGCTTGACAAATTTGAAGGAACACCGAAGATTAAGTCTT 480
QY 481 CAAATCATACATCCGCTTAACTAGAACAAATATTCGCAAAAGCTCCGGAACCGTGG 540
DB 481 CAACATCAACATCCCTTCTAATCTCGAACGATCTTCTGCAAAAGCCGGAACCAATGG 540
QY 541 GTTCCTCATTTCAAGTCTCTTTCATGATGCTGACAGATGACAGATGGAGG 600
DB 541 GTTCCTCATTTCCGTTGATCATTTATCAATGTTCCGTTGTTATGCAAGATGGAGT 600
QY 601 GATTAATTTTCGAGAGCGGTGACGCTGCGCCGCGGATAGACCTGTAATGATCATGTC 660
DB 601 GAGACATTTTCGAGAGGGGTTCGCTGCGCGCGGGAAGAACTTATTAATGATCATGTC 660
QY 661 GAGGTGATTCAGAAACAGGAGAGAGATGTGGCGGTGCTGTTAGGCCCAATATAT 720
DB 661 GAAGGTGATTCAGAAACCGGAGAGACAAATGTGGCTGCTGCAATTAAGACCAATATAT 720
QY 721 CTCAGTGAACACCTAGACTTCAATGTCAGTCTTCTGAAATGATGTCAGTAAAGTAT 780
DB 721 TTGAGCGGTATTTGACCTTAATTCACGTCTTATTCACGAGTGAATACAGCTC 780
QY 781 ATTGATGACATCCGACCGCATTAATCTAAAGCTAAAGCATGAAAGATTCGTGGGGCC 840
DB 781 ATTGAGACATTAAGCCCAATTAATTTGAATTAAGCATGAAAGCACTAATTTGGGGCA 840
QY 841 CAGAAAGATTGGCAATTAATTTGCAATGACGTAAAGCATTCATAATTAAGCGGATC 900
DB 841 CAAAGGACCTGGCAATTAATCTGTAATATGAAAGCGGTTCATAATTAAGGAGATTA 900
QY 901 CCAAGCATCGTCTTTCATCTGTCAGTGAAGGTGTCAGTATTAAGAGTCTTATAGACAA 960
DB 901 CCATCATCTGTTGTTCATTCAGTGAAGGTTCAGTATTAAGAGTCTTCTGACAAA 960
QY 961 GCAGAAATACAGGTCTCAAGAACTGACTATCAAGATCGATCTTCATCACCCTACA 1020
DB 961 GAAGAAACCGAGCTTACCACTGACTATTCATATGATGATCTTCGACACCTCACA 1020
QY 1021 GCCCCTCTATCAAGAGACACACAGCAAGCCAA 1056
DB 1021 GCCCCTCTATCAAGACACACAGATTTGCCAA 1056

RESULT 13
US-10-633-850-79
Sequence 79, Application US/10633850
Publication No. US20040205843A1
GENERAL INFORMATION:
APPLICANT: Hanley-Bowdoin, Linda
APPLICANT: Orozco, Beverly M.
APPLICANT: Griseem, Wilhelm
TITLE OR INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
FILE REFERENCE: 5051.4581P
CURRENT APPLICATION NUMBER: US/10/633,850
PRIOR FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 09/289,346
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 60/125,004
NUMBER OF SEQ ID NOS: 112
SOFTWARE: Patent version 3.2
SEQ ID NO 79
LENGTH: 1056
TYPE: DNA
ORGANISM: Tomato golden mosaic virus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1056)
OTHER INFORMATION: TGMV AL1 K144 mutant
US-10-633-850-79

Query Match 56.1%; Score 607.4; DB 18; Length 1056;

Best Local Similarity 73.7%; Pred. No. 6e-177;
Matches 773; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

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QY 5 CCCACCAAGAAATTGAGTTCAGTCAAGAACTATTTCTTAATTTATCCCAAGTCT 64
DB 8 CGCATCCAAAACGGTTTCAATATAATGCAAAAATTTTCTTACATATCTCAGTCT 67
QY 65 CTCTATTTAAAGAAAGCACTTTCCCAATTCAAAACTTAATATCCCAAGTCAAGA 124
DB 68 CCTGTGCAAGAAAGTCACTTTCTCAATTCAGAGCCCTTAACACCTCGATTAAACAAA 127
QY 125 AATTCAATCAAAATTTGAGAGCTTCATGAAAATGGGGAACCTCATCTCATGCTTG 184
DB 128 AATTCAATCAAAATTTGAGAGCTTCATGAAAATGGGGAACCTCATCTCATGCTTG 187
QY 185 TTGAGTTGGAAGTAAAGTACCAATGACGAATTAACAGATTCTTGAGCTGGTCCCAA 244
DB 188 TTGAGTTGGAAGTAAAGTACCTGCGCAAAATCAAGATTCTTGAGCTGGTATCCCAA 247
QY 245 CCGGTCAGACATTTTCATCCGAATTTTCAGGAGCTTAAATGAGCTCCGAGCTCAAT 304
DB 248 CAAGGTGAGACATTTTCATCCGAATTTTCAGGAGCTTAAATGAGCTCCGAGCTCAAG 307
QY 305 CATACATCGACAAAGAGCGAGATACCAATCGAATGGGGAATTTCCAAATGAGCGGAGAT 364
DB 308 GGTACATCGACAAAGAGCGAGATATCTGTATGGGGAATTTCCAGGTGAGCGGTCGAA 367
QY 365 CTGCGACAGAGGCGACAGCTGCTGCTAATGATTTGCAATGCGAAAGCTTAATGAGCTT 424
DB 368 GTGCTAGAGAGGTGCGCAAAATCTTAACGAGCTGACGAGAGGCTTAAATGCTTTCTT 427
QY 425 CGGTTCAATGCTTACCGGTTCTAAGGGAACCAACCAAGATTGTGATTACAAA 484
DB 428 CCGGGAAGAGCGCTGCAATATTAAGAGAAAATCCAGAAAATATTTATTTAGT 487
QY 485 ATCAATACATCCGCTTAACCTAGAAAGAAATTTGCAAGAGCTCGGGAACCGGAGTTC 544
DB 488 TCACAAATCTTAATGCAATTTAGATATGATTTGATTAAGATCTCGAAACCATATGCTTC 547
QY 545 CTCATTTCAAGTCTCTTTCTTCACTAAGCTTCTGAGAGATGCAAGAAATGGGCGATA 604
DB 548 CTCGTTTCAAGTCTCTTCACTAAGCTTCTGAGAGATGCAAGAAATGGGCGATA 607
QY 605 ATTAATTTGGGAGCGGAGCTGCGGCGCGGAGTAAAGCTGTAATGATCATGCTGAGG 664
DB 608 ATTAATTTGGGAGCGGAGCTGCGGCGCGGAGTAAAGCTGTAATGATCATGAGG 667
QY 665 GTGATTCAGAAACAGGGAAGCAATGAGGCGGCTGCTAAGGCGCCATTAATCTCA 724
DB 668 GCGATGAGTGGAGGGAAGCAATGAGGCGGCTGCTAAGGCGCCATTAATCTCA 727
QY 725 GTGAGACCTAGACTTCAATGAGTCTTCTGAAATGATGTCATATTAAGCTCATTTG 784
DB 728 GCGGAGCTTTGGAATCTCAATTTCTAGGTTTACTCAAAAGGTTGATTAAGCTCATTTG 787
QY 785 ATGACATCGACCGGACTTATCTAAAGCTAAAGCACTGGAAGAAATGCTGGGCGCCAGA 844
DB 788 ATGATGTCACACGCAATATCTAAAGTTGAAACATTTGGAAGAACTATTTGGGCGCCAAA 847
QY 845 AAGTTGGGCAATCAATTTGCAAGTAAAGCTTAAGCGAGTCAAAATTAAGGCGGAATCCAG 904
DB 848 GAGTTTGGGCAATCAATTTGCAAGTAAAGCTTAAGCGAGTCAAAATTAAGGCGGAATCCAGT 907
QY 905 CAATCGTCTTTGCAATCTGAGAGGCTGCAAGCTTAAGAGATTCTTGAACAAAGCAG 964
DB 908 CAATCGTCTTTGCAATCTGAGAGGCTGCTAATTAAGTTTCTCTGACAAAGAGG 967
QY 965 AAAATACAGGTCTCAAGAACTGAGACTATCAAGAAATGCAATCTTATCACTCAGAGCC 1024
DB 968 AAAACATCTCACTAAAGAACTGAGCTTTCAATATGGAATTCGTTCTCTCAATCTCC 1027
QY 1025 CCGCTATCAAGAGAGCAAGCAAGC 1053
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DB 1028 CCGCTATCAAGAGCTCAACAGAGAGCAGC 1056

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RESULT 14
US-10-633-850-83
; Sequence 83. Application US/10633850
; Publication No. US20040205843A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Griseem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633, 850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 83
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1056)
; OTHER INFORMATION: TMV AL1 E146 mutant
US-10-633-850-83
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Query Match 56.1%; Score 607.4; DB 18; Length 1056;
Best Local Similarity 73.7%; Pred. No. 6e-177;
Matches 773; Conservative 0; Mismatches 276; Indels 0; Gaps 0;

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QY 5 CCCACCAAGAAATTGAGTTCAGTCAAGAACTATTTCTTAATTTATCCCAAGTCT 64
DB 8 CGCATCCAAAACGGTTTCAATATAATGCAAAAATTTTCTTACATATCTCAGTCT 67
QY 65 CTCTATTTAAAGAAAGCACTTTCCCAATTCAAAACTTAATATCCCAAGTCAAGA 124
DB 68 CCTGTGCAAGAAAGTCACTTTCTCAATTCAGAGCCCTTAACACCTCGATTAAACAAA 127
QY 125 AATTCAATCAAAATTTGAGAGCTTCATGAAAATGGGGAACCTCATCTCATGCTTG 184
DB 128 AATTCAATCAAAATTTGAGAGCTTCATGAAAATGGGGAACCTCATCTCATGCTTG 187
QY 185 TTGAGTTGGAAGTAAAGTACCAATGACGAATTAACAGATTCTTGAGCTGGTCCCAA 244
DB 188 TTGAGTTGGAAGTAAAGTACCTGCGCAAAATCAAGATTCTTGAGCTGGTATCCCAA 247
QY 245 CCGGTCAGACATTTTCATCCGAATTTTCAGGAGCTTAAATGAGCTCCGAGCTCAAT 304
DB 248 CAAGGTGAGACATTTTCATCCGAATTTTCAGGAGCTTAAATGAGCTCCGAGCTCAAG 307
QY 305 CATACATCGACAAAGAGCGAGATACCAATCGAATGGGGAATTTCCAAATGAGCGGAGAT 364
DB 308 GGTACATCGACAAAGAGCGAGATATCTGTATGGGGAATTTCCAGGTGAGCGGTCGAA 367
QY 365 CTGCGACAGAGGCGACAGCTGCTGCTAATGATTTGCAATGCGAAAGCTTAAATGAGCTT 424
DB 368 GTGCTAGAGAGGTGCGCAAAATCTTAACGAGCTGCAAGAGGCTTAAATGAGCTTCTT 427
QY 425 CCGTTCAATCTGCTTAAAGCTTCAAGGAGTAAAGCAACCAAGAAATTTGTAATTAACAA 484
DB 428 CCAAGAGAGAGCGCTGCAAGATTAATTAAGAGAAAATCCAGAAAATATTTATTTCACT 487
QY 485 ATCAATACATCCGCTTAACTTAAGCAATTAATGCAAGAGCTCCGGAACCGTGGCTTC 544
DB 488 TCACAAATCTTAATTAAGCAATTTAGATGAGATATTTGATTAAGATCTCTGGAACATGCTTC 547
QY 545 CTCATTTCAAGTCTCTTTCTTCACTAAGCTTCGAGAGATGCAAGAAATGGGCGGATA 604
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Dh 548 CTCGGTTCAGTCTCATCTTACTTAACGTCGACGAGATGAGCAATAGGGCTGAAA 607
Qy 605 ATATATTCGGAGCGGGTGAAGCGTCCGCCGAGTAAAGCTGTAAATCATCTGTCAGG 664
Dh 608 ATATATTTGGAAAAGTTCCGCTGGCGGCGGAGAACCTATTAATTAATCATCTGAGG 667
Qy 665 GTGATTCAGAAACAGGAGACGATGTGGGCGCTGGCTTAAGGCCCATTAATCATCTCA 724
Dh 668 GCGATACGCGAGCGGAAAGACTATGTGGCTCCTTACAGGCCCATTAATTAATTTGA 727
Qy 725 GTGACACCTAGACTTCAATGTGCAAGTCTTCTGAAATGATGTGCAATTAACGTCAATG 784
Dh 728 GCGGGCATTTGGATCTCAATTTCTAGGGTTTACTCAAAAGGTTAGATTAACGTCAATG 787
Qy 785 ATGACATCGCACCGCATTTATCTTAAGCTTAAGCACTGAAAAGAAATTCGTGGGGCCCA 844
Dh 788 ATGATGTCAACCGCAATATCTTAAGTTGAAACATTTGAAAGAACTAATGGGGCCCA 847
Qy 845 AAGATTGGCAATCAATTTGCAAGTACGCTTAAGCAGTTCAAAATTAAGCGGAATCCCA 904
Dh 848 GAGATTGGCAGACTTAATCTTAATTAACGAAAGCCAGTTCAAAATTAAGAGATATCCCGT 907
Qy 905 CAATCGTCTTTGCAATCTGTGAGGGTGCAGCTTAATAAGCTTTTGAACAAGCAG 964
Dh 908 CAATCGTCTGTGCAATCTGTGAGGGTGTGCTAATAAGTTTCTCTGCAACAAGAGG 967
Qy 965 AAAATTAAGGTCTCAAAATCTGAATCTTAACAAGATTTGATCTTATCACTCAAGCCC 1024
Dh 968 AAAACACTTCACTTAATAAAGCTGACCTTCAATAATGGAATTCGTCTTCAACTCCC 1027
Qy 1025 CCCTCTATCAAGAGACACAGGCAAGC 1053
Dh 1028 CCCTCTATCAAAAGCTCAACACAGAGCAGC 1056

RESULT 15
US-10-633-850-50
; Sequence 50, Application US/10633850
; Publication No. US20040205843A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Grubisem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 50
; LENGTH: 1056
; TYPE: DNA
; ORGANISM: Tomato golden mosaic virus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1056)
; OTHER INFORMATION: TGMV AL1 coding sequence
US-10-633-850-50

Query Match 55.9%; Score 605.8; DB 18; Length 1056;
Best Local Similarity 73.6%; Pred. No. 1.9e-176;
Matches 772; Conservative 0; Mismatches 277; Indels 0; Gaps 0;

Qy 5 CCCACCAAGAAATTAAGATTGAGTCAAGCAATTAATCTTCTTAATCTTATCCAGAGCT 64
Dh 8 CGCATCCAAAGCGTTTCAATTAATGCAAAATTTTCTTACATATCTCAAGTCT 67
Qy 65 CTCTATTAAGAAGAAAGCACTTCCCAATTAACAAACCTAAATACCCAGTCAACAGA 124

Dh 68 CCTGTCCAAAGAAATCACTTTCTCTCAATTAACAAGCCCTAAACACTCCGATTAACAAA 127
Qy 125 AATTTCATCAAAATTTGAGAGAGCTTCAATGAATAATGGGAAACCTCATCTCATGTGTTG 184
Dh 128 AATTTCATCAAAATTTGAGAGAGCTTCAATGAATAATGGGAAACCTCATCTCATGTGTTA 187
Qy 185 TTGAGTTCAAGAGTAAGTACCAATGACAGAAATACAGATTTCTTGAAGCTGCTCCCAA 244
Dh 188 TTGAGTTCAAGAGTAAGTACCAATGACAGAAATCAAGATTTCTTGAAGCTGCTCCCAA 247
Qy 245 CCGGTCAGACATTTTCATCCGAATTTGAGAGAGTCAATGAGCTCCGACGTCAAT 304
Dh 248 CAAGGTACAGACATTTTCATCCGAATTTGAGAGAGTCAATGAGCTCCGACGTCAAG 307
Qy 305 CATATATCGCAAGAGAGAGATTAATCAATGCAATGGGGAATTTCCAAATGAGCGGAGAT 364
Dh 308 CATATATCGCAAGAGAGAGATTAATCAATGCAATGGGGAATTTCCAAATGAGCGGAGAA 367
Qy 365 CTGACAGAGAGGCGAGCAGTCTGTATGATTCATATGCGAAAGCATTAATGCAAGTT 424
Dh 368 GTGTCAGAGAGGTTGCGCAACATCTTACAGACGCTGACAGAGGCTTAATGCTTCTT 427
Qy 425 CGGTTCAATCTGCTTAGCGGTTCTTAAGGAGAAACCAACAAAGATTTTGTATTAACA 484
Dh 428 CCAAGAGAGAGGCTTGCAGATTAATTAAGAGAAATCCAGAAATATTTATTTCACT 487
Qy 485 ATATATCATCCGCTCAATCTTAAGAGATTTTCCGAAGGCTCCGGAACCGGAGTTC 544
Dh 488 TCACAAATCTTAATTAAGATTAATTAAGATTTTGAAGTCTTCAACATGAGCTTC 547
Qy 545 CTCATTTCAAGTCTCTTCTTCACTTAACCTTCTGACGAGATGCAAGATGGGCGGATA 604
Dh 548 CTCGTTCCAGTCTCTATCATTTAATCTTACGTGCAAGAGAGATTAATGAGTGGCTGAA 607
Qy 605 ATATATTCGGAAGGAGTACGCTGCGCGCGGATTAAGCTGTAATGATCTGTCAGG 664
Dh 608 ATATATTTGGAAGAGTTCGCTGCGCGCGGAGAGACCTATTAATGATCTGTCAGG 667
Qy 665 GTGATTCAGAAACAGGGAAGACGATGTGGGCGGTGTTAGGCCCATTAATCATCTCA 724
Dh 668 GCGATAGTCCGAGGGAAGACTATGTGGCTGTGTACTAGGCCCATTAATTAATTTGA 727
Qy 725 GTGACACCTAGACTTCAATGTGCAAGTCTTCTGCAATGATGTGCAATTAACGTCAATG 784
Dh 728 GCGGCAATTTGATCTCAATTTAGGTTTACTCAAAAGGTTGATTAACGTCAATG 787
Qy 785 ATGACATCGCACCGCATTTATCTTAAGCTTAAGCACTGAAAAGAAATTCGTGGGGCCCA 844
Dh 788 ATGATGTCAACCGCAATATCTTAAGTTGAAACATTTGAAAAGAACTCATTTGGGGCCCA 847
Qy 845 AAGATTGGCAATCAATTTGCAAGTACGCTTAAGCAGTTCAAAATTAAGGGGGAATCCCA 904
Dh 848 GAGATTGGCAGACTTAATCTTAATTAAGGAAAGCCAGTTCAAAATTAAGGAGATTCCTG 907
Qy 905 CAATCGTCTTTGCAATCTGTGAGGGTGCAGCTTAATAAGTCTTGAACAAGCAG 964
Dh 908 CAATCGTCTGTGCAATCTGTGAGGGTGTGCTAATAAGTCTTCTGCAACAAGAGG 967
Qy 965 AAAATTAAGGTCTCAAGAACTGAATCTTAAGAATGAGATTTCTTATCACTCAAGCCC 1024
Dh 968 AAAACACTTCACTTAATAAAGCTGACCTTCAATAATGGAATTCGTCTTCAACTCCC 1027
Qy 1025 CCCTCTATCAAGAGACACAGGCAAGC 1053
Dh 1028 CCCTCTATCAAGCTCAACACAGAGCAGC 1056

Search completed: December 4, 2004, 17:49:13
Job time : 633 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: December 4, 2004, 13:14:20 ; Search time 3903 Seconds
(without alignments)
10111.255 Million cell updates/sec

Title: US-09-491-063a-1

Perfect score: 1083
Sequence: 1 atgcccccccaagaat.....gcaatcagaagcgacaggt 1083

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

EST: *
1: gb_est1: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	47.2	4.4	636	B2394806	B2394806 E1NB009TF
C 2	43.2	4.0	977	CNS0405K	AL268481 Tetradon
C 3	41.8	3.9	791	CO088898	CO088898 GR_Ea08B
C 4	41	3.8	864	AO891340	AO891340 HS_3143_A
C 5	40.8	3.8	822	CNS011PO	AL100566 Drosophila
C 6	40.4	3.7	609	BM370082	BM370082 BM370082
C 7	40.4	3.7	685	AV957294	AV957294 AV957294
C 8	40.4	3.7	697	CNS018M5	AL109511 Drosophila
C 9	39.8	3.7	607	BP764040	BP764040 BP764040
C 10	39.8	3.7	739	BX262586	BX262586 BX262586
C 11	39.6	3.7	2433	CNS0A7F8	BX823251 Arabidops
C 12	39.6	3.6	738	BX200121	BX200121 Dario rer
C 13	39.4	3.6	762	CC375636	CC375636 PUM234TB
C 14	39.4	3.6	933	BZ826521	BZ826521 PUGC117TD
C 15	39.4	3.6	945	CG168857	CG168857 PUFROV4TB
C 16	38.6	3.6	640	AO254323	AO254323 CP60765B
C 17	38.6	3.6	1102	CNS01521	AL104916 Drosophila
C 18	38.4	3.5	1310	CNS0152M	AL106118 Drosophila
C 19	38.2	3.5	700	BUS25743	BUS25743 603742692
C 20	38	3.5	615	BM300507	BM300507 WCA053B12
C 21	38	3.5	723	CL593149	CL593149 OB_Ba005
C 22	38	3.5	849	CC504462	CC504462 CH240_344
C 23	38	3.5	911	CC092222	CC092222 CSU-K34.1
C 24	38	3.5	939	CNS00CNG	AL059400 Drosophila

25	37.6	3.5	784	5	BUS26709	603610148
26	37.6	3.5	1145	7	CK161861	CK161861 FAS01443
C 27	37.4	3.5	477	5	BY249188	BY249188 BY249188
28	37.4	3.5	546	5	BP033725	BP033725 BP033725
29	36.6	3.4	713	5	BU443152	BU443152 604144395
C 30	36.6	3.4	740	5	CC120153	CC120153 NDL_73M13
C 31	36.6	3.4	783	9	BX145514	BX145514 Dario rer
C 32	36.6	3.4	854	8	B21413	B21413 T14124-5p6
C 33	36.4	3.4	535	9	CR313399	CR313399 Medicago
C 34	36.4	3.4	693	8	BZ07541	BZ07541 h59c08.b
C 35	36.4	3.4	818	6	CD439694	CD439694 E01N0527
C 36	36.4	3.4	829	9	CC919532	CC919532 t025a11b
C 37	36.4	3.4	836	9	CG267577	CG267577 OXK071TH
38	36.4	3.4	920	9	CG197027	CG197027 PUFMO55TD
C 39	36.4	3.4	931	9	CG074022	CG074022 PUHO83TD
C 40	36.4	3.4	954	9	CG197026	CG197026 PUFMO55TB
C 41	36.2	3.3	445	8	CC054409	CC054409 SALK_0601
C 42	36.2	3.3	483	9	BX167127	BX167127 Dario rer
C 43	36.2	3.3	733	6	CA946220	CA946220 000271 BO
C 44	36.2	3.3	930	9	BX966641	BX966641 Forward B
C 45	36	3.3	418	5	BU711438	BU711438 SJAAME09

ALIGNMENTS

RESULT 1
LOCUS B2394806/c 636 bp DNA linear GSS 30-APR-2003
DEFINITION E1NB009TF E1_10_12_KB Entamoeba invadens genomic clone E1NB009,
genomic survey sequence.
ACCESSION B2394806
VERSION B2394806.1 GI:30241347
KEYWORDS
SOURCE Entamoeba invadens
ORGANISM Entamoeba invadens
REFERENCE Wang,Z., Samuelson,J., Clark,C.G., Eichinger,D., Paul,J., van
Dellen,K., Hall,N., Anderson,I. and Loftus,B.
Gene discovery in the Entamoeba invadens genome
Mol. Biochem. Parasitol. 129 (1), 23-31 (2003)
MEDLINE 22684048
PUBMED 12798503
COMMENT Other GSSs: E1NB009TR
Contact: Brendan Loftus
Department of Eukaryotic Genomics
TIGR
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-838-3543
Fax: 301-838-0208
Email: enta@tigr.org
DNA was provided by Daniel Eichinger
Seq primer: TF
Clase: sheared ends.
Location/Qualifiers
1..636
/organism="Entamoeba invadens"
/mol_type="genomic DNA"
/strain="E1P-1"
/db_xref="taxon:33085"
/clone="E1NB009"
/clone_1ib="E1_10_12_KB"
/note="Vector: pHO52; Site 1: Batx1; Total genomic DNA was
isolated from early log phase trophozoites of E. invadens
IP-1 using a Qiagen plant DNA extraction kit. A shotgun
medium-size plasmid library (average insert size of 10 -
12 kb) was generated by random mechanical shearing of E.
invadens genomic DNA, repairing the ends of DNA fragments
with T4 Polymerase, adding Batx1 adaptors and ligating
into the Batx1 site of a pUC-derived vector pHO52."

ORIGIN

Query Match 4.4%; Score 47.2; DB 8; Length 636;
Best Local Similarity 50.4%; Pred. No. 0.015;
Matches 115; Conservative 0; Mismatches 113; Indels 0; Gaps 0;

QY 12 AAAGAAATTTAGAGTTCAGTCAAGAACTATTTCTTAAGTTATCCCGAGTCTCTATC 71
DB 284 AAAACCTTCAGATTAACGGAAGAACTGCTCTTAACATGCGACAGACACCTCTCC 225
QY 72 TAAAGAAAGAGCACTTCCCAATTAACAAACCTTAATACCCCACTCAACAGAAATTCAT 131
DB 224 AAAAGAAAGAGCACTTCCCAATTAACAAACCTTAATACCCCACTCAACAGAAATTCAT 165
QY 132 CAAATTTGAGAGAGCTTCATGAATGAGGAACCTCATCTCCATGCTGTTGTTAGT 191
DB 164 AGTCGTGTCAGAGAAAAACGAAAAAGAGGACCTGATCTTACATGAGTGTAAAGCT 105
QY 192 CGAAGGTAGTACCAATGACGAATTAACAGATTCTTGACCTGCTC 239
DB 104 GGAAGAAAGATATGTTTCAGAGATCAGAGCTGCTGAATCTTAAGCTC 57

RESULT 2
CNS0405K/ 977 bp DNA linear GSS 01-SEP-2000
LOCUS
DEFINITION Tetradon nigroviridis genome survey sequence T7 end of clone
071D12 of library G from Tetradon nigroviridis, genomic survey
sequence.
ACCESSION AL268481.1 GI:7990330
VERSION
KEYWORDS GSS; genome survey sequence.
SOURCE Tetradon nigroviridis
ORGANISM Tetradon nigroviridis
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthopterygia; Acanthopterygii; Percomorpha; Tetraodontiformes;
Tetraodontidae; Tetraodontidae; Tetradon.
REFERENCE 1
AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,
Bernot, A., Fizames, C., Mincker, P., Broctier, P., Quetier, F.,
Saurin, W., and Weissenbach, J.
TITLE BSLMATE of human gene number provided by genome-wide analysis
using Tetradon nigroviridis DNA sequence
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)
MEDLINE 20296633
PUBMED 10835645
REFERENCE 2
AUTHORS Roest Crolius, H., Jaillon, O., Dasilva, C., Ozouf-Coetzee, C.,
Fizames, C., Fischer, C., Bouneau, L., Billault, A., Quetier, F.,
Saurin, W., Bernot, A., and Weissenbach, J.
TITLE Characterization and repeat analysis of the compact genome of the
freshwater pufferfish Tetradon nigroviridis
JOURNAL Genome Res. 10 (7), 939-949 (2000)
MEDLINE 20359837
PUBMED 10899143
REFERENCE 3
AUTHORS Genoscope.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :
BP 131 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
COMMENT This sequence is a single read and was generated as part of a large
scale clone-end sequencing project of the Tetradon nigroviridis
genome. For more information, please take a look at
http://www.genoscope.cns.fr/Tetradon.
FEATURES
Source
1. .977
/organism="Tetradon nigroviridis"
/mol_type="genomic DNA"
/db_xref="taxon:99883"
/clone="071D12"
/clone_1b="G"
/note="Genoscope sequence ID : COB071DB06DP1-end : T7"

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Best Local Similarity 57.4%; Pred. No. 0.27;
Matches 78; Conservative 0; Mismatches 58; Indels 0; Gaps 0;

QY 97 CAAACCTTAATATCCCGAGTCAACAGAAATTCATCAAAATTTGACAGAGCTTCATGA 156
DB 485 CAAATCTAATTTCCCATTCAAATGATATGATTTATGTAACAGATTAATACA 426
QY 157 AATGGGAACCTCATCTCCATGCTGTTGTTCAAGTTAAGTACATGACGAAT 216
DB 425 GCGTTGGAGAGCAAGCTTCGATGATGATGATGATGATGATGATGATGATGATGAT 366
QY 217 AACGATTCCTTGACC 232
DB 365 GAGCTATTAATCTCTCC 350

RESULT 3
CO088898/ 791 bp mRNA linear EST 16-JUN-2004
LOCUS
DEFINITION GR_Ea08B20.r GR_Ea Gossypium raimondii cDNA clone GR_Ea08B20 3',
mRNA sequence.
ACCESSION CO088898
VERSION
KEYWORDS EST.
SOURCE Gossypium raimondii
ORGANISM Gossypium raimondii
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids II; Malvales; Malvaceae; Malvoideae; Gossypium.
REFERENCE 1 (bases 1 to 791)
AUTHORS Kim, H., Yu, Y., Kudrna, D., Hatfield, J., Stum, D., Mueller, C.,
Udall, J. A., Rapp, R. A., Wendel, J. F., Rao, K., Soderlund, C. and
Wing, R. A.
TITLE Global assembly of cotton ESTs
JOURNAL Unpublished (2004)
COMMENT Contact: Rod A. Wing
Arizona Genomics Institute
The University of Arizona
Forbes Building Room 303, Tucson, AZ, 85721-0036, USA
Tel: 520 626 9595
Fax: 520 621 1259
Email: http://genome.arizona.edu
plate: 08 row: B column: 20.
FEATURES
Source
1. .791
/organism="Gossypium raimondii"
/mol_type="mRNA"
/db_xref="taxon:29730"
/clone="GR_Ea08B20"
/tissue_type="whole seedlings"
/dev_stage="first true leaves"
/lab_host="DH10B"
/clone_1b="GR_Ea"
/note="Vector: PCMV.SPORT-6.1; Site 1: NotI; Site 2:
EcoRV. Library made by Invitrogen with RNA supplied by
Wendle lab. Directional cloned into NotI-EV. Colonies
plated/picked by Agt. More glycerol clones held in -80."

ORIGIN
Query Match 3.9%; Score 41.8; DB 7; Length 791;
Best Local Similarity 51.9%; Pred. No. 0.68;
Matches 94; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 847 GATTGCAATCAATTCAGTACGATGATGATGATGATGATGATGATGATGATGATGAT 906
DB 651 GAGTGGGCAACAGGATATGACAGATATTAACCTTCAATCAATTAAGGCGATCAAGAG 592
QY 907 ATCGTCTTGCAATCTCTGTGAGGATGATGATGATGATGATGATGATGATGATGATGAT 966
DB 591 TTAACTGTAACATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 532

ORIGIN


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QY 967 AATACAGTCTCAAGAACTGACTATCAAGATGCAATCTTCATACCTTCAGACCC 1026
DB 531 GTCAAGGCTCGGGACCGGACAAATTAGATGCACTTATCAAGACTTACTGCTCC 472
QY 1027 C 1027
DB 471 C 471

RESULT 4
A0891340/c 864 bp DNA linear GSS 10-NOV-1999
LOCUS HS_3143_A1_C01_T7C CIT Approved Human Genomic Sperm Library D Homo
DEFINITION sapiens genomic clone Plate=3143 Col=1 Row=E, genomic survey
sequence.
ACCESSION A0891340
VERSION A0891340.1 GI:6347530
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
1 (bases 1 to 864)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
10448764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@reagen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3143 row: E column: 1
Seq primer: T7
Class: BAC ends
High quality sequence stop: 864.
FEATURES
source
1. 864
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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/sex="male"
/clone_1lb="CIT Approved Human Genomic Sperm Library D"
/notes="Organ: sperm; Vector: pBelobAC11; BAC clones in
E-Coli DH10B"
ORIGIN
Query Match 3.8%; Score 41; DB 8; Length 864;
Best Local Similarity 50.8%; Pred. No. 1.2;
Matches 98; Conservative 0; Mismatches 95; Indels 0; Gaps 0;
QY 205 CAATGCAGAAATTAACAGATTCTTGAGCTGTCTCCCAACCGGTACGACATTTCCAT 264
DB 590 CACTGATACAAAATGCAATCTTCATCTTAGTATCCCAAAAGCCCTCTTAATCTTCC 531
QY 265 CCGAATATTCAGGAGGATTAATCGAGCTCCGACGCTCAATCATCATGCAAGAGCGA 324
DB 530 TTGACTGTGAACGGGCTAGATTACATCCAAATTTATATATATCTCTTATTTAGGGC 471
QY 325 GATACAAATGCAATGGAGATTTTCAAAATGACGCGAGATCTGCGAGAGAGGCCAGAG 384
DB 470 TTATATTAACCTGTCTGAAGATGACTAGTAGAGGAGGTTTTCAGTAGAGGAGTAA 411
QY 385 TCTGCTAATGATT 397

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DB 410 TCAGCAAAACGTT 398

RESULT 5
CNS011PO/c 822 bp DNA linear GSS 26-JUL-1999
LOCUS BACN06K06 of DrosBAC library from Drosophila melanogaster (fruit
DEFINITION fly), genomic survey sequence.
ACCESSION AL100566
VERSION AL100566.1 GI:5612177
KEYWORDS GSS.
SOURCE Drosophila melanogaster (fruit fly)
ORGANISM Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 822)
REFERENCE Genoscope.
AUTHORS Direct Submission
TITLE Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
JOURNAL BP 191 9106 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
COMMENT Determination of this BAC-end sequence was carried out as part of a
collaboration with the European Drosophila Genome Project (EDGP) -
http://www.edgp.edi.ac.uk -. This Drosophila melanogaster BAC
library (Dros BAC) was made by Alain Billaud at CEPH (Centre
d'Etude du Polymorphisme Humain) with funding provided by a MRC
project grant. The DNA was prepared from embryos by Alain Bucheton
and Genevieve Payan. It has been constructed in the vector
pBelobAC11.
FEATURES
source
1. 822
/organism="Drosophila melanogaster"
/mol_type="genomic DNA"
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ORIGIN
Query Match 3.8%; Score 40.8; DB 9; Length 822;
Best Local Similarity 39.0%; Pred. No. 1.4;
Matches 96; Conservative 29; Mismatches 121; Indels 0; Gaps 0;
QY 6 CCGACAAAGAAATTTAGAGTTGAGTCAAGCAAGACTATTCCTTAATCCAGTCTC 65
DB 773 YCCCCAAAATAATTCATAATTAACTTAACTTAACTTAACTTAACTTAACTTAACTTAA 714
QY 66 TCTATCTAAAGAAAGAGACTTCCCAATTACAAACCTTAATACCCAGTCAACAGAA 125
DB 713 AAMATTAAATBBSAATAATCCSATTAATTTSSSATTAATCCAAATATYASCCMAAAA 654
QY 126 ATTATCAAAATTTGCAAGAGCTTCATGAAAATGGGAACTCATCTCATGTCTGT 185
DB 653 CMCACAAACAAATTTCAAGCATATMAATATSMATATSSCATTAATATCGACACAAAATSTTCGT 594
QY 186 TCACTGCAAGATTAATCAATCAATGCAAGCAATTAACAGATCTTGAGCTGTCTCCCAAC 245
DB 593 TAGCGTCAATSAANAAGSCCAAAATSAATSMATCAATSCAATCAATGATTTSTSMASMTS 534
QY 246 CCGGTC 251
DB 533 CACCTC 528

RESULT 6
BM370082/c 609 bp mRNA linear EST 28-MAY-2004
LOCUS BM370082 Yutaka Satou unpublished cDNA library, mature adult whole
DEFINITION animal Clona intestinalis cDNA clone c1m849d15 5', mRNA sequence.

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ACCESSION      BM370082
VERSION        BM370082.1
KEYWORDS       GI:47785910
SOURCE
ORGANISM       Ciona intestinalis
REFERENCE
AUTHORS        Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
TITLE          Phlebobranchia; Cloniidae; Ciona.
JOURNAL        1 (bases 1 to 609)
COMMENT        Satou,Y., Shin-i,T., Kohara,Y. and Satoh,N.
               Expressed genes in Ciona intestinalis (2004)
               Unpublished (2004)
               Contact: Yutaka Satou
               Department of Zoology
               Kyoto University
               Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
               Tel: 81-75-753-4095
               Fax: 81-75-705-1113
               Email: yutaka@acidian.zool.kyoto-u.ac.jp.

FEATURES
source
1..609
/organism="Ciona intestinalis"
/mol_type="mRNA"
/db_xref="taxon:7719"
/clone="cima849d15"
/tissue_type="whole animal"
/dev_stage="mature adult"
/clone_lib="Yutaka Satou unpublished cDNA library, mature
adult whole animal"

ORIGIN
Query Match      3.7%; Score 40.4; DB 5; Length 609;
Best Local Similarity 53.9%; Pred. No. 1.7;
Matches 83; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

OY 681 GAAGCAGATGCGGGCGCGCTTGAGGCCACATATCATCTCAGTGCACCTGACTT 740
    |||||
DB 274 GAAGATTGTTTCATTGATTCCTTACACAATGATTCCTGTCAGTGGAAACGACTT 215
    |||||
OY 741 CAATGTCGAGTCTTCTCGAATGATGTCACGATTAACGTCAATTGATGACATCGCACCGCA 800
    |||||
DB 214 TAATGTCGGGTGCTCTTAAACGATGGGGAGGTCACGCCATATGCAAGTTGCACACACA 155
    |||||
OY 801 TTATCTAAGCTAAGCAGCTGSAAGATTTGCTG 834
    |||||
DB 154 TTATATGAACCTTAATTAATATGCAATCGTTAATG 121
    |||||

RESULT 7
AV957294/c 665 bp mRNA linear EST 14-MAR-2002
LOCUS AV957294 Nori Satoh unpublished cDNA library, egg Ciona
DEFINITION Intestinalis cDNA clone c1eg14g03 5', mRNA sequence.
ACCESSION AV957294
VERSION AV957294.1
KEYWORDS GI:19445593
SOURCE EST.
ORGANISM Ciona intestinalis
Ciona intestinalis
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
Phlebobranchia; Cloniidae; Ciona.
1 (bases 1 to 665)
Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@acidian.zool.kyoto-u.ac.jp.
Location/Qualifiers
1..665
/organism="Ciona intestinalis"

```

[illegible]

Db	560	TGGAAMAAAAAACAATCTCTMTATATATAAAATTAATAATTYYTMYNNHAAAAMAAAM	501
Oy	132	CAAAATTGCAGAGCGTTTCATGAAABAGGGGAACCTCATCTCCATGTGCTTGTCAGTT	191
		:::::	
Db	500	AAMWMAATATATATATATAABABATATATATATATATAGACRYCATATATCTTGATCAGA	441
Oy	192	CGAAGGTAGTACCAGATCGACGAATPAACGATTTCTGCAC	231
Db	440	TCAATAGCCGAATCGATCTAGTACTGTCCGTTGCCGC	401
RESULT 9			
LOCUS	BP764040/c	607 bp	mRNA EST 10-JUL-2004
DEFINITION	BP764040 mouse (C57BL/6) pancreatic islet library with recombination-based method Mus musculus cDNA clone mic30074 3', mRNA sequence.		
ACCESSION	BP764040		
VERSION	BP764040.1	GI:50222738	
KEYWORDS	EST.		
SOURCE	Mus musculus (house mouse)		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 607) Nishimura,M., Yokoi,N., Miki,T., Horikawa,Y., Yoshioke,H., Takeda,J., Ohara,O. and Seino,S. Construction of a multi-functional cDNA library specific for mouse pancreatic islets and its application to microarray		
AUTHORS	Unpublished (2004)		
TITLE	Contact: Susumu Seino Division of Cellular and Molecular Medicine Kobe University Graduate School of Medicine 7-5-1 Kusunoki-cho, Chuo-ku, Kobe, Hyogo 650-0017, Japan Tel.: 81-78-382-5360 Fax: 81-78-382-5370 Email: seinodom@kobe-u.ac.jp.		
JOURNAL			
COMMENT	Location/Qualifiers		
FEATURES			
source	1..607		
	/organism="Mus musculus"		
	/mol_type="mRNA"		
	/strain="C57BL/6"		
	/db_xref="taxon:10090"		
	/clone="mic30074"		
	/sex="male"		
	/tissue_type="pancreatic islet"		
	/dev_stage="adult"		
	/clone_lib="mouse (C57BL/6) pancreatic islet library with recombination-based method"		
ORIGIN			
Query Match	3.7%	Score 39.8;	DB 5; Length 607;
Best Local Similarity	55.4%;	Pred. No. 2.6;	
Matches	97;	Conservative	0; Mismatches 77; Indels 1; Gaps 1
Oy	738	CTTCAATSGTCGAGCTCTTCGAAAGATGTCAGATATAACGTCATGTATGACATCGACC	797
Db	180	CTTCATGCGTATATGAATATTTATTAATGTGGAATPAACATTTTCATTTTATGATCACAGC	121
Oy	798	GCAATTATCTAAAGCTAAAGCACTGGAAGAATTCGTGGGGGCCAGAAAGATTTGCCAATC	857
Db	120	TCAGTTCCTTAATAGAAACGAACTGTAA--CCTATCTGCAGACCAAGCAAAGGCACAATA	62
Oy	858	AAATTGCAAGTAGCGTAGCCAGTCCAATTAAAGCGGAATCCAGCAATGCTG	912
Db	61	AAACTGGAAGTGAAMAAAAAAAAAAAAAAAAAAAGCGCGCCGACGCTTCTTG	7
RESULT 10			
LOCUS	BX262586	739 bp	mRNA linear EST 24-MAY-2004
DEFINITION	BX262586 AGENAE Gallus gallus multi-tissues normalized and		

ACCESSION	onec-subtracted cDNA library (gcal) Gallus gallus cDNA clone gcal0008c.h.19 5prim, mRNA sequence.
VERSION	BX62586
KEYWORDS	BX62586.1 GI:28585184
SOURCE	EST.
ORGANISM	Gallus gallus (chicken)
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
AUTHORS	Heraut,F., Le Meuth-Metzinger,V., Desert,C., Retout,E., PlumI,F., Klopp,C. and Douaire,M.
TITLE	Construction and primary characterization of chicken normalized multi-tissue cDNA libraries
JOURNAL	multi-tissue cDNA libraries
COMMENT	Unpublished (2003) INRA, UMR INRA-ENSAE Genetique Animale Contact: Douaire M Tel: +33 (0) 2.23.48.54.63 Fax: +33 (0) 2.23.48.54.70 Email: Madeleine.Douaire@cazon.inra.fr Sequence cleaned of vector, adaptor and repetitions. Contact us at sigenahupport@jouy.inra.fr to obtain the chromatogram of this sequence. Plate: 0008 row: h column: 19 Seq primer: M13R.
FEATURES	Location/Qualifiers
source	1..739 /organism="Gallus gallus" /mol_type="mRNA" /db_xref="taxon:9031" /clone="gcal0008c.h.19" /tissue_type="multi-tissues" /dev_stage="from embryos to adults" /lab_host="MDH10B" /clone_lib="AGENAS Gallus gallus multi-tissues normalized and once-subtracted cDNA library (gcal)" /note="Vector: pRTD-pac; tissues: adipose tissue, brain, kidney, liver, multi-tissues, muscle, ovary, testis, bone marrow, caecum, duodenum, embryos, fabricius gland, granulosa, hypothalamus, ileon, jejunum, oviduct, pancreas, skin, spleen, thymus, utero-vaginal gland, pituitary gland, hematopoietic progenitor cells, small follicle. Clone distribution : AGENAS Resource centre. Francois PIUMI, Francois.PIumi.inra.fr, INRA, CEA Radiobiologie et Etude du genome (LREG), Domaine de Vilvert, 78352, Jouy-en-Josas cedex, FRANCE"
ORIGIN	
Query Match	3.7%; Score 39.8; DB 5; Length 739;
Best Local Similarity	49.8%; Pred. No. 2.7;
Matches 101; Conservative	0; Mismatches 102; Indels 0; Gaps 0
Dy	382 CAGTCTGCTAATGATTCATATGCAAGAAGCATTAATGCAGGTGGTTCAATTGCTCTTA 441
Db	231 CAGGTGGTGCTTATTTCTGATTTAAAGCAAACGCTTGGAAGAACTGAGAAAGCTGCATCA 290
Oy	442 GCGGTTCTAAGGAGAAACAACCAAAAGATTTTGATTAACAATAATCATAACATCCGCTCT 501
Db	291 AGTCTCAAAATGAGAAAAACCAAAAGACTAATCTTCTAAGAAACATTTAACAACTTCT 350
Oy	502 AACCTAGAACAAATTTGCAAAAGGCTCCGGAACCGTGAGTTCTCTCATTTCAAGTCTCT 561
Db	351 GACCCTGTGCCCTTAATTCACAGACTCCCTGGCAAGTAGATTTTCTCACACTCCCTTTACT 410
Oy	562 TCTTTCACTAAGTTCCTGACGA 584
Db	411 GCTTCCAAATATGCTGCAGTGA 433

LOCUS CNS0A7F8 2433 bp mRNA linear HTC 06-FEB-2004
 DEFINITION Arabidopsis thaliana Full-length cDNA Complete sequence from clone
 GSLTSL16F06 of Adult vegetative tissue of strain col-0 of
 Arabidopsis thaliana (thale cress).

ACCESSION BX823253.1 GI:42466155
 VERSION BX823253
 KEYWORDS HTC; GSLT cDNA.
 SOURCE Arabidopsis thaliana (thale cress)
 ORGANISM Arabidopsis thaliana

REFERENCE
 AUTHORS Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 1 (bases 1 to 2433)
 Castelli, V., Aury, J.M., Jallion, O., Wincker, P., Clepet, C.,
 Menard, M., Cruaud, C., Querier, F., Scarpelli, C., Schachter, V.,
 Temple, G., Caboche, M., Weissenbach, J. and Salanoubat, M.
 Whole Genome Sequence Comparisons and 'Full-length' cDNA Sequences:
 A Combined Approach to Evaluate and Improve Arabidopsis Genome
 Annotation
 Unpublished
 2 (bases 1 to 2433)
 Genoscope.
 Direct Submission
 Submitted (18-NOV-2003) Genoscope - Centre National de Sequencage :
 BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
 - Web : www.genoscope.cns.fr)
 The sequences are based on single pass reads.
 Life Technologies (a division of Invitrogen) members carried out
 full-length libraries construction : Temple G.
 Genoscope members carried out sequencing and annotation : Castelli
 V., Aury J.M., Jallion O., Wincker P., Menard M., Cruaud C.,
 Schachter V., Weissenbach J., Salanoubat M.
 UNIV INRA : Clepet C., Caboche M.
 Annotation is based on the June 2003 version of the Arabidopsis
 genome released by MIPS (Munich Information Center for Protein
 Sequences) . 5 prime and 3 prime are assembled with Phrap.
 http://www.genoscope.cns.fr/externe/sequences/Banque_Projet_SF/Full
 length
 http://www.genoscope.cns.fr/cgi-bin/ggb/ggb?source=Arabidopsis.

FEATURES
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 /mol_type="mRNA"
 /strain="Col-0"
 /db_xref="taxon:3702"
 /clone="GSLTSL16F06"
 /tissue_type="Adult vegetative tissue"
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 complement(1..2433)
 /gene="At3g15220"

ORIGIN
 gene
 3.7%: Score 39.6; DB 3; Length 2433;
 Best Local Similarity 48.6%: Pred. No. 4.1;
 Matches 108; Conservative 0; Mismatches 114; Indels 0; Gaps 0;

Query Match 250 TCAGCATTTCATCCGATATTCAGAGAGTAAATCGAGCTCCGACATCAATCTAC 309
 1613 TCAGAGATTCAGCAAGCAATCTCGGAGAGCAAGCAGACCTCGAGCAAGTTTACA 1672
 310 ATCGACAGAGCAGAGATACATCGAATGGGAGATTTCCAAATCGACGAGATCTGCC 369
 1673 AAGGGTAAAGATAGAAAGAGTTGGAATGGAATAATCAATATGATGGGAAGTTAAC 1732
 370 AAGAGAGGCGACAGCTGCTATGATTCATATGCGAAGCATTAATGACAGTTGCGTT 429
 1733 AAGAGAGGAGGAGCAATGCGAATGATTCGATTCATTCAGAAATTCGCGCATTAAGTCT 1792
 430 CAATTCGCTTAAGGCTTAAAGGAGCAACCAACAAAGT 471
 1793 AGTAAACAAAAGTAGTTCCAGAGTCCAGAACAGTAGTAGT 1834

RESULT 12
 LOCUS BX200121 738 bp DNA linear GSS 29-JAN-2003
 DEFINITION Danio rerio genomic clone DKEX-210B11, genomic survey sequence.
 ACCESSION BX200121
 VERSION BX200121.1 GI:28032007
 KEYWORDS GSS.
 SOURCE Danio rerio (zebrafish)
 ORGANISM Danio rerio

REFERENCE
 AUTHORS Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;
 Cypriniformes; Cyprinidae; Danio.
 1 (bases 1 to 738)
 Humphray, S.J., Huckle, E. and Durham, J.L.
 Direct Submission
 Submitted (27-JAN-2003) The Sanger Institute, Wellcome Trust Genome
 Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
 humphrey@sanger.ac.uk Unpublished
 This sequence was generated from the SP6 end of BAC 210B11. 210B11
 is part of the Daniokey BAC library created by R. Plasterk and N.V.
 Keygene. Further details:
 http://www.sanger.ac.uk/projects/D_rerio/
 Location/Qualifiers

FEATURES
 source
 1..738
 /organism="Danio rerio"
 /mol_type="genomic DNA"
 /db_xref="taxon:7955"
 /clone="DKEX-210B11"
 /tissue_type="testis"
 /note="vector pindigobAC-536"

ORIGIN
 Query Match 13 MAGAATTAGAGTTCAGTCAAGAACTATTTCTTAATCCAGCTGCTCTATCT 72
 Best Local Similarity 54.5%: Score 39.4; DB 9; Length 738;
 Matches 79; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Query 568 AAGTATATTAGATTATATATATCAATTTATTTATTAATACATGTGCTCATAT 627
 73 AAGAGAGACACTTTCCCAATTACAAACCTAATATCCCACTCAACAGAAATTCATC 132
 628 AAACCAATTAATTAATACATATTTATTCATGCTTCTTTGAAAAAACCACAA 687
 133 AAAATTGCAGAGGCTTCATGAAA 157
 688 AACGTAAAGTTAAAGTTATAGAAA 712

RESULT 13
 LOCUS CC375636 762 bp DNA linear GSS 19-MAY-2003
 DEFINITION PUMH234TB ZM_0.6_1.0_KB Zea mays genomic clone ZMHBTA488E20,
 genomic survey sequence.
 ACCESSION CC375636
 VERSION CC375636.1 GI:30849253
 KEYWORDS GSS.
 SOURCE Zea mays
 ORGANISM Zea mays

REFERENCE
 AUTHORS Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
 clade; Panicoideae; Andropogoneae; Zea.
 1 (bases 1 to 762)
 Whiteley, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,
 Resnick, A., Fraser, C.M., Yuan, Y., San Miguel, P., Ma, J. and
 Bennetzen, J.
 Maize Genomics Consortium
 Unpublished (2003)
 Other GSS: PUMH234TD
 Contact: Cathy Whiteley
 TIGR
 9712 Medical Center Drive, Rockville, MD 20850, USA
 Tel: 301-838-5843

Tue Dec 7 11:29:39 2004

us-09-491-063a-1.rst

Page 8

Search completed: December 4, 2004, 16:15:44
Job time : 3911 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2004, 14:54:43 ; Search time 157 Seconds
(without alignments)
824.849 Million cell updates/sec

Title: US-09-491-063a-2

Sequence: 1 MPEPKKRVQSKNYFLTPQ.....PLYQESTQASQETGNKQAG 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*

1: geneseqp1960s:*\n2: geneseqp1990s:*\n3: geneseqp2000s:*\n4: geneseqp2001s:*\n5: geneseqp2002s:*\n6: geneseqp2003as:*\n7: geneseqp2003bs:*\n8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match Length	DB ID	Description
1	1908	98.4	361	2	AAW34336 Tomato mo
2	1902	98.1	361	2	AAW34325 Tomato mo
3	1892	97.6	361	2	AAW34326 Tomato mo
4	1879	96.9	361	2	AAW34324 Tomato mo
5	1575	81.2	353	1	AAW34332 Bean gold
6	1572	81.1	353	2	AAW34332 Bean gold
7	1572	81.1	353	2	AAW34338 Bean gold
8	1567	80.8	353	2	AAW34333 Bean gold
9	1566	80.7	353	2	AAW34335 Bean gold
10	1564	80.7	353	2	AAW34335 Bean gold
11	1499	77.3	356	3	AAW34337 Tomato ye
12	1308.5	67.5	359	2	AAW34330 Tomato ye
13	1305.5	67.3	359	2	AAW34330 Tomato ye
14	1305.5	67.3	359	2	AAW34330 Tomato ye
15	1293.5	66.7	357	2	AAW34329 Tomato ye
16	1293.5	66.7	357	2	AAW34329 Tomato ye
17	1290.5	66.6	357	2	AAW34330 Tomato ye
18	1286.5	66.6	357	2	AAW34331 Tomato ye
19	1262	65.1	362	2	AAW34331 Tomato ye
20	1242	64.1	361	1	AAW34327 Tomato mo
21	599	30.9	142	6	AAW34327 Tomato mo
22	486	25.1	142	6	AAW34327 Tomato mo
23	486	25.1	142	6	AAW34327 Tomato mo
24	277	14.3	292	3	AAW34317 Maatrevir
25	260	13.4	264	3	AAW34317 Maatrevir

26	260	13.4	264	3	AAW34336 standard; protein; 361 AA.
27	257	13.3	264	8	AAW34336 standard; protein; 361 AA.
28	241	12.4	143	3	AAW34336 standard; protein; 361 AA.
29	224	11.6	70	3	AAW34336 standard; protein; 361 AA.
30	224	11.6	70	3	AAW34336 standard; protein; 361 AA.
31	218	11.2	70	3	AAW34336 standard; protein; 361 AA.
32	217	11.2	70	3	AAW34336 standard; protein; 361 AA.
33	216	11.1	70	3	AAW34336 standard; protein; 361 AA.
34	216	11.1	70	3	AAW34336 standard; protein; 361 AA.
35	214	11.0	70	3	AAW34336 standard; protein; 361 AA.
36	214	11.0	70	3	AAW34336 standard; protein; 361 AA.
37	212	10.9	70	3	AAW34336 standard; protein; 361 AA.
38	210	10.8	70	3	AAW34336 standard; protein; 361 AA.
39	210	10.8	70	3	AAW34336 standard; protein; 361 AA.
40	209	10.8	70	3	AAW34336 standard; protein; 361 AA.
41	208	10.7	70	3	AAW34336 standard; protein; 361 AA.
42	207	10.7	70	3	AAW34336 standard; protein; 361 AA.
43	200	10.3	70	3	AAW34336 standard; protein; 361 AA.
44	141	7.3	27	2	AAW34336 standard; protein; 361 AA.
45	137	7.1	27	2	AAW34336 standard; protein; 361 AA.

ALIGNMENTS

RESULT 1	AAW34336	AAW34336 standard; protein; 361 AA.
ID	AAW34336	AAW34336 standard; protein; 361 AA.
AC	AAW34336	AAW34336 standard; protein; 361 AA.
XX	AAW34336	AAW34336 standard; protein; 361 AA.
DT	17-OCT-2003 (revised)	AAW34336 standard; protein; 361 AA.
DT	27-APR-1998 (first entry)	AAW34336 standard; protein; 361 AA.
XX	AAW34336	AAW34336 standard; protein; 361 AA.
DE	Tomato mottle virus AC1 protein.	AAW34336 standard; protein; 361 AA.
XX	Tomato mottle virus AC1 protein.	AAW34336 standard; protein; 361 AA.
KW	Geminivirus; TOMOV; AC1 gene; transdominant mutation; transgenic plant; disease resistance.	AAW34336 standard; protein; 361 AA.
XX	Tomato mottle virus; isolate Florida.	AAW34336 standard; protein; 361 AA.
OS	Tomato mottle virus; isolate Florida.	AAW34336 standard; protein; 361 AA.
XX	Tomato mottle virus; isolate Florida.	AAW34336 standard; protein; 361 AA.
PN	MO9739110-AL.	AAW34336 standard; protein; 361 AA.
XX	MO9739110-AL.	AAW34336 standard; protein; 361 AA.
PD	23-OCT-1997.	AAW34336 standard; protein; 361 AA.
XX	23-OCT-1997.	AAW34336 standard; protein; 361 AA.
PF	15-APR-1997; 97MO-US006300.	AAW34336 standard; protein; 361 AA.
XX	15-APR-1997; 97MO-US006300.	AAW34336 standard; protein; 361 AA.
PR	16-APR-1996; 96US-0015517P.	AAW34336 standard; protein; 361 AA.
XX	16-APR-1996; 96US-0015517P.	AAW34336 standard; protein; 361 AA.
PA	(SEMT-) SEMINIS VEGETABLE SEEDS INC.	AAW34336 standard; protein; 361 AA.
PA	(WISC) WISCONSIN ALUMNI RES FOUND.	AAW34336 standard; protein; 361 AA.
XX	(SEMT-) SEMINIS VEGETABLE SEEDS INC.	AAW34336 standard; protein; 361 AA.
PI	Scout UT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;	AAW34336 standard; protein; 361 AA.
XX	Scout UT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;	AAW34336 standard; protein; 361 AA.
DR	WPI; 1997-526447/48.	AAW34336 standard; protein; 361 AA.
XX	WPI; 1997-526447/48.	AAW34336 standard; protein; 361 AA.
PT	N-PDB; AAT93294.	AAW34336 standard; protein; 361 AA.
PT	N-PDB; AAT93294.	AAW34336 standard; protein; 361 AA.
PT	Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant	AAW34336 standard; protein; 361 AA.
PT	geminivirus - have increased resistance to geminivirus infection e.g. tomato	AAW34336 standard; protein; 361 AA.
PT	mottle virus, tomato yellow leaf curl virus or bean golden mosaic	AAW34336 standard; protein; 361 AA.
PT	geminivirus.	AAW34336 standard; protein; 361 AA.
XX	Example 3.3; Page 57-58; 132pp; English.	AAW34336 standard; protein; 361 AA.
XX	Example 3.3; Page 57-58; 132pp; English.	AAW34336 standard; protein; 361 AA.
CC	This protein comprises the wild-type AC1 protein of tomato mottle virus	AAW34336 standard; protein; 361 AA.
CC	(TOMOV), a geminivirus that has a bipartite genome. The AC1 gene (see	AAW34336 standard; protein; 361 AA.
CC	AAW34336) must be expressed for efficient replication of the two genomic	AAW34336 standard; protein; 361 AA.
CC	components, DNA-A and DNA-B. The AC1 protein has a DNA binding site	AAW34336 standard; protein; 361 AA.
CC	specific to the DNA-A common region, a DNA nicking activity, and an ATP	AAW34336 standard; protein; 361 AA.
CC	binding activity. The invention involves production of transgenic plants	AAW34336 standard; protein; 361 AA.
CC	containing DNA comprising AC1 or CI wild-type or mutant sequences that	AAW34336 standard; protein; 361 AA.
CC	negatively interfere in trans with geminiviral replication during	AAW34336 standard; protein; 361 AA.
CC	infection. Such transgenic plants are resistant to viral infection. The	AAW34336 standard; protein; 361 AA.

CC AC1/C1 genes are especially from TOMOV, tomato yellow leaf curl virus or
 CC bean golden mosaic geminivirus (see AAT93282-93) and encode polypeptides
 CC (see AAM34324-35) that have mutations in the highly conserved DNA-nicking
 CC domain and/or the NTP-binding domain. (Updated on 17-Oct-2003 to
 CC standardise OS field)

XX Sequence 361 AA;

Query Match 98.4%; Score 1908; DB 2; Length 361;
 Best Local Similarity 98.4%; Pred. No. 4.5e-169;
 Matches 355; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPPPKRRVOSKXVFLTYPPQCSLSKEBALSQLNLNTPVKKFKIKICREIHENGEPHLHV 60
 DB 1 MPPPKRRVOSKXVFLTYPPQCSLSKEBALSQLNLNTPVKKFKIKICREIHENGEPHLHV 60
 QY 61 LVQEGKYQCTNNRFPDLVSPTRSAHPHPNIQAKSSDVKSYIDKDGDTIEWGDFQIDG 120
 DB 61 LVQEGKYQCTNNRFPDLVSPTRSAHPHPNIQAKSSDVKSYIDKDGDTIEWGDFQIDG 120
 QY 121 RSARGGQOSANDSYAKALNAGVSQALAVLREBPQKDFVLQNNHNRSLERIFAKAPEPW 180
 DB 121 RSARGGQOSANDSYAKALNAGVSQALAVLREBPQKDFVLQNNHNRSLERIFAKAPEPW 180
 QY 181 VPPFQVSSFTNVPEDEMOMADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTWABALGPHNY 240
 DB 181 VPPFQVSSFTNVPEDEMOMADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTWABALGPHNY 240
 QY 241 LSGHLDNNGRVFNSNDVQYVNIIDIAHPHYLKLKHKMKELGAKQKQMSCKYKGPVQIKGSI 300
 DB 241 LSGHLDNNGRVFNSNDVQYVNIIDIAHPHYLKLKHKMKELGAKQKQMSCKYKGPVQIKGSI 300
 QY 301 PAIVLCNPGEGASVKEFLDKAENTGLKNMTIKNAIFITLTAPLYOESTQASOETGNQKQ 360
 DB 301 PAIVLCNPGEGASVKEFLDKAENTGLKNMTIKNAIFITLTAPLYOESTQASOETGNQKQ 360
 QY 361 G 361
 DB 361 G 361

RESULT 2
 AAM34325
 ID AAM34325 standard; protein; 361 AA.

XX AAM34325;

XX 27-APR-1998 (first entry)

XX Tomato mottle virus AC1 mutant TOMV-AC1d1m1.

XX Geminiivirus; TOMOV-AC1d1m1; AC1 gene; transdominant mutation;

XX transgenic plant; disease resistance.

XX Tomato mottle virus; isolate Florida.

XX Synthetic.

XX WO9739110-A1.

XX 23-OCT-1997.

XX 15-APR-1997; 97WO-US006300.

XX 16-APR-1996; 96US-0015517P.

XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.

XX (WISC) WISCONSIN ALUMNI RES FOUND.

XX Stout UT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;

XX WPI, 1997-526447/48.

XX N-PSDB; AAT93283.

PT Transgenic plants expressing geminivirus AC1 and C1 wild-type and mutant
 PT genes - have increased resistance to geminivirus infection e.g. tomato
 PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
 PT geminivirus.

XX Example 3.5; Page 64-65; 132pp; English.

XX This protein comprises a transdominant lethal mutant, designated TOMOV-
 CC AC1d1m1, of tomato mottle virus (TOMOV) AC1 protein (see AAM34336). It is
 CC encoded by a mutant AC1 gene (see AAT93283) of tomato mottle virus.
 CC (TOMOV), and carries a mutation in an NTP-binding domain. The AC1 gene
 CC (see also AAT93294) must be expressed for efficient replication of the
 CC two genomic components, DNA-A and DNA-B, of the bipartite TOMOV genome.
 CC The invention involves production of transgenic plants containing DNA
 CC comprising geminivirus AC1 or C1 wild-type or mutant sequences that
 CC negatively interfere in trans with geminiviral replication during
 CC infection. Such transgenic plants are resistant to viral infection. The
 CC AC1/C1 genes are especially from TOMOV, tomato yellow leaf curl virus or
 CC bean golden mosaic geminivirus (see AAT93282-93) and encode polypeptides
 CC (see AAM34324-35) that have mutations in the highly conserved DNA-nicking
 CC and/or NTP-binding domains

XX Sequence 361 AA;

Query Match 98.1%; Score 1902; DB 2; Length 361;
 Best Local Similarity 98.1%; Pred. No. 1.6e-168;
 Matches 354; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 MPPPKRRVOSKXVFLTYPPQCSLSKEBALSQLNLNTPVKKFKIKICREIHENGEPHLHV 60
 DB 1 MPPPKRRVOSKXVFLTYPPQCSLSKEBALSQLNLNTPVKKFKIKICREIHENGEPHLHV 60
 QY 61 LVQEGKYQCTNNRFPDLVSPTRSAHPHPNIQAKSSDVKSYIDKDGDTIEWGDFQIDG 120
 DB 61 LVQEGKYQCTNNRFPDLVSPTRSAHPHPNIQAKSSDVKSYIDKDGDTIEWGDFQIDG 120
 QY 121 RSARGGQOSANDSYAKALNAGVSQALAVLREBPQKDFVLQNNHNRSLERIFAKAPEPW 180
 DB 121 RSARGGQOSANDSYAKALNAGVSQALAVLREBPQKDFVLQNNHNRSLERIFAKAPEPW 180
 QY 181 VPPFQVSSFTNVPEDEMOMADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTWABALGPHNY 240
 DB 181 VPPFQVSSFTNVPEDEMOMADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTWABALGPHNY 240
 QY 241 LSGHLDNNGRVFNSNDVQYVNIIDIAHPHYLKLKHKMKELGAKQKQMSCKYKGPVQIKGSI 300
 DB 241 LSGHLDNNGRVFNSNDVQYVNIIDIAHPHYLKLKHKMKELGAKQKQMSCKYKGPVQIKGSI 300
 QY 301 PAIVLCNPGEGASVKEFLDKAENTGLKNMTIKNAIFITLTAPLYOESTQASOETGNQKQ 360
 DB 301 PAIVLCNPGEGASVKEFLDKAENTGLKNMTIKNAIFITLTAPLYOESTQASOETGNQKQ 360
 QY 361 G 361
 DB 361 G 361

RESULT 3
 AAM34326
 ID AAM34326 standard; protein; 361 AA.

XX AAM34326;

XX 27-APR-1998 (first entry)

XX Tomato mottle virus AC1 mutant TOMV-AC1d1m23.

XX Geminiivirus; TOMOV-AC1d1m23; AC1 gene; transdominant mutation;

XX transgenic plant; disease resistance.

XX Tomato mottle virus; isolate Florida.

XX Synthetic.

PN MO9739110-A1.
 XX AAW34324
 PD 23-OCT-1997.
 XX
 XX 15-APR-1997; 97MO-US006300.
 PF
 XX 16-APR-1996; 96US-0015517P.
 PR
 XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX
 PI Scout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
 DR WPI, 1997-526447/48.
 DR N-PSDB; AAT93284.
 XX
 PT Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
 PT genes - have increased resistance to geminivirus infection e.g. tomato
 PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
 PT geminivirus.
 XX
 XX Example 3.6; Page 67-69; 132pp; English.
 PS
 XX This protein comprises a transdominant lethal mutant, designated ToMoV-
 CC AC1d1m23, of tomato mottle virus (ToMoV) AC1 protein (see AAW34336). It
 CC is encoded by a mutant AC1 gene (see AAT93284) of tomato mottle virus
 CC virus (ToMoV), and carries 2 mutations in an NTP-binding domain. The AC1
 CC gene (see also AAT93294) must be expressed for efficient replication of
 CC the two genomic components, DNA-A and DNA-B, of the bipartite ToMoV
 CC genome. The invention involves production of transgenic plants containing
 CC DNA comprising geminivirus AC1 or CI wild-type or mutant sequences that
 CC negatively interfere in trans with geminiviral replication during
 CC infection. Such transgenic plants are resistant to viral infection. The
 CC AC1/CI genes are especially from ToMoV, tomato yellow leaf curl virus or
 CC bean golden mosaic geminivirus (see AAT93282-93) and encode polypeptides
 CC (see AAW34324-35) that have mutations in the highly conserved DNA-nicking
 CC and/or NTP-binding domains
 XX
 XX Sequence 361 AA;
 SQ
 Query Match 97.6%; Score 1892; DB 2; Length 361;
 Best Local Similarity 97.8%; Pred. No. 1.4e-167;
 Matches 353; Conservative 3; Mismatches 5; Indels 0; Gaps 0;
 QY 1 MPPPKFRVQSKYFLTYPCSLSKERALSQLOLNTTPVKKFKIKICREIHENGEPHLAV 60
 DB 1 MPPPKFRVQSKYFLTYPCSLSKERALSQLOLNTTPVKKFKIKICREIHENGEPHLAV 60
 QY 61 LVQFEGKYQCTNNRFPDLVSPTRSAHFHPIIOGAKSSDVKSYYIDKDGDTIEWGDFQIDG 120
 DB 61 LVQFEGKYQCTNNRFPDLVSPTRSAHFHPIIOGAKSSDVKSYYIDKDGDTIEWGDFQIDG 120
 QY 121 RSARGGQGSANDSYAKALNAGSVQALAVIREOPKDFVLQNNHINSNLERIPAKAPBPW 180
 DB 121 RSARGGQGSANDSYAKALNAGSVQALAVIREOPKDFVLQNNHINSNLERIPAKAPBPW 180
 QY 181 VPPFQVSSFTNVDPDEMOMADNYFGTGDAAPPRPVSIIIEGDSRTGKTMMARALGPHNY 240
 DB 181 VPPFQVSSFTNVDPDEMOMADNYFGTGDAAPPRPVSIIIEGDSRTGKTMMARALGPHNY 240
 QY 241 LSGHLDPNNGVFPNDVQYNIYIDIAFHYLKLKWKELLAGQKQWQSNCKYGPQVIGGI 300
 DB 241 LSGHLDPNNGVFPNDVQYNIYIDIAFHYLKLKWKELLAGQKQWQSNCKYGPQVIGGI 300
 QY 301 PATVLCPNPGGASKEYEFLDKAENTGLKNMTIKNAIFITLLTAPLYQESTQASOETGNQKQ 360
 DB 301 PATVLCPNPGGASKEYEFLDKAENTGLKNMTIKNAIFITLLTAPLYQESTQASOETGNQKQ 360
 QY 361 G 361
 DB 361 G 361

RESULT 4
 AAW34324
 ID AAW34324 standard; protein, 361 AA.
 XX
 XX AAW34324;
 AC
 XX 27-APR-1998 (first entry)
 DT
 XX Tomato mottle virus AC1 mutant ToMoV-AC1d1m.
 XX
 XX Geminivirus; ToMoV-AC1d1m; AC1 gene; transdominant mutation;
 KM transgenic plant; disease resistance.
 XX
 XX Tomato mottle virus; isolate Florida.
 OS Synthetic.
 XX
 XX MO9739110-A1.
 XX
 XX 23-OCT-1997.
 PD
 XX 15-APR-1997; 97MO-US006300.
 PF
 XX 16-APR-1996; 96US-0015517P.
 PR
 XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX
 PI Scout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
 DR WPI, 1997-526447/48.
 DR N-PSDB; AAT93282.
 XX
 XX Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
 PT genes - have increased resistance to geminivirus infection e.g. tomato
 PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
 PT geminivirus.
 XX
 XX Example 3.4; Page 60-62; 132pp; English.
 PS
 XX This protein comprises a transdominant lethal mutant, designated ToMoV-
 CC AC1d1m, of tomato mottle virus (ToMoV) AC1 protein (see AAW34336). It is
 CC encoded by a mutant AC1 gene (see AAT93282) of tomato mottle virus
 CC virus (ToMoV), and carries 3 mutations in its NTP-binding domains. The AC1 gene
 CC (see also AAT93294) must be expressed for efficient replication of the
 CC two genomic components, DNA-A and DNA-B, of the bipartite ToMoV genome.
 CC The invention involves production of transgenic plants containing DNA
 CC comprising geminivirus AC1 or CI wild-type or mutant sequences that
 CC negatively interfere in trans with geminiviral replication during
 CC infection. Such transgenic plants are resistant to viral infection. The
 CC AC1/CI genes are especially from ToMoV, tomato yellow leaf curl virus or
 CC bean golden mosaic geminivirus (see AAT93282-93) and encode polypeptides
 CC (see AAW34324-35) that have mutations in the highly conserved DNA-nicking
 CC and/or NTP-binding domains
 XX
 XX Sequence 361 AA;
 SQ
 Query Match 96.9%; Score 1879; DB 2; Length 361;
 Best Local Similarity 97.2%; Pred. No. 2.3e-166;
 Matches 351; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 1 MPPPKFRVQSKYFLTYPCSLSKERALSQLOLNTTPVKKFKIKICREIHENGEPHLAV 60
 DB 1 MPPPKFRVQSKYFLTYPCSLSKERALSQLOLNTTPVKKFKIKICREIHENGEPHLAV 60
 QY 61 LVQFEGKYQCTNNRFPDLVSPTRSAHFHPIIOGAKSSDVKSYYIDKDGDTIEWGDFQIDG 120
 DB 61 LVQFEGKYQCTNNRFPDLVSPTRSAHFHPIIOGAKSSDVKSYYIDKDGDTIEWGDFQIDG 120
 QY 121 RSARGGQGSANDSYAKALNAGSVQALAVIREOPKDFVLQNNHINSNLERIPAKAPBPW 180
 DB 121 RSARGGQGSANDSYAKALNAGSVQALAVIREOPKDFVLQNNHINSNLERIPAKAPBPW 180
 QY 181 VPPFQVSSFTNVDPDEMOMADNYFGTGDAAPPRPVSIIIEGDSRTGKTMMARALGPHNY 240

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Db      181 VPPQVSSFTNVPEEMEMADNFTGTGAARPERPVSIIVEGDSRTGHTMMARALGPHNY 240
Qy      241 LSGHLDNGRVFSNDVQYNNVDDIAPHYLKIKHMKELGAKQKQMSCKTGKPVQIKGI 300
Db      241 LSGHLDNGRVFSNDVQYNNVDDIAPHYLKIKHMKELGAKQKQMSCKTGKPVQIKGI 300
Qy      301 PAIVLCNPGGASGYKEFLDKAENTGLKNMTIKNAIFITLAPLYQESTQASQEQGNQAK 360
Db      301 PAIVLCNPGGASGYKEFLDKAENTGLKNMTIKNAIFITLAPLYQESTQASQEQGNQAK 360
Qy      361 G 361
Db      361 G 361

RESULT 5
AAP70407
ID AAP70407 standard; protein, 353 AA.
XX
AC AAP70407;
XX
XX 25-MAR-2003 (revised)
DT 02-MAY-1991 (first entry)
XX
DE ORF 4 gene product of Bean Golden Mosaic virus.
XX
XX Plant vector.
XX
XX Bean golden mosaic virus.
XX
XX JP61257186-A.
XX
XX 14-NOV-1986.
XX
XX 10-MAY-1985; 85JP-00098108.
XX
XX 10-MAY-1985; 85JP-00098108.
XX
XX (TEIJU) TEIJUN LTD.
XX
XX WPI; 1987-159662/23.
DR N-PSDB; AAN70630.
XX
XX New DNA and hybrid DNA - used for recombinant vector of plants.
PT
XX
XX Disclosure; Fig 6; 24pp; Japanese.
XX
XX The sequence encoding this protein may be taken along with the -a DNA
CC sequence and a suitable resistance gene, and used to create a recombinant
CC plant vector. See also AAN70629. (Updated on 25-MAR-2003 to correct PA
CC field.)
XX
XX Sequence 353 AA;
SQ
Query Match 81.2%; Score 1575; DB 1; Length 353;
Best Local Similarity 79.8%; Pred. No. 5.4e-138;
Matches 281; Conservative 34; Mismatches 37; Indels 0; Gaps 0;

Qy      1 MPPPKFRVOSKNYFLTYPOCSLSKEBALSQLQNTLPVKKFKIKIRELHENGEPHLAV 60
Db      1 MPPPKFRVOSKNYFLTYPRCTIPKEALSQLOKIHHTTNKKFKIVCEBRHDNBPFLHA 60
Qy      61 LVQFEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKQGDITEMQDPQIDG 120
Db      61 LIQEGFKICTNKLFDLVSTTRSAHFHPNIQAKSSDVKSYIDKQGVITEWQFOVDG 120
Qy      121 RSARGGQOSANDSYAKALNAGVSQALAVLREQPKDFVLQNHVIRSNLERIFAKAPEPW 180
Db      121 RSARGGQOSANDSYAKALNADISALTLTKEQPKDFVLQNHVIRSNLERIFKVPBEPW 180
Qy      181 VPPQVSSFTNVPEEMEMADNFTGTGAARPERPVSIIVEGDSRTGHTMMARALGPHNY 240

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Db      181 VPPPLSSFVNIPVWQMDWYDFGSGAARPERPVSIIVEGDSRTGHTMMARALGPHNY 240
Qy      241 LSGHLDNGRVFSNDVQYNNVDDIAPHYLKIKHMKELGAKQKQMSCKTGKPVQIKGI 300
Db      241 LSGHLDNRSRVSVSVSNVYNNVDDISPNYLKIKHMKELGAKQKQMSCKTGKPVQIKGI 300
Qy      301 PAIVLCNPGGASGYKEFLDKAENTGLKNMTIKNAIFITLAPLYQESTQASQ 352
Db      301 PSIVLCNPGGSSYKDFLNKEENRALHNTIHNAPFTLAPLYQSTADQDQ 352

RESULT 6
AAM34332
ID AAM34332 standard; protein, 353 AA.
XX
XX AAM34332;
XX
XX 17-OCT-2003 (revised)
DT 27-APR-1998 (first entry)
XX
DE Bean golden mosaic geminivirus CI BGA190 mutant.
XX
XX Geminivirus; BGMY; CI gene; transdominant mutation; transgenic plant;
XX disease resistance.
XX
XX Bean golden mosaic virus; type II isolate Guatemala.
XX
XX W09739110-A1.
XX
XX 23-OCT-1997.
XX
XX 15-APR-1997; 97WO-US006300.
XX
XX 16-APR-1996; 96US-0015517P.
XX
XX (SEMI-) SEMINIS VEGETABLE SEEDS INC.
PA (WISC) WISCONSIN ALUMNI RES FOUND.
XX
XX Stout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
PI
XX WPI; 1997-526447/48.
DR N-PSDB; AAT93290.
XX
XX Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
PT genes - have increased resistance to geminivirus infection e.g. tomato
PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
PT geminivirus.
XX
XX Example 5; Page 103-105; 132pp; English.
XX
XX This protein comprises a control mutant of the bean golden mosaic virus
CC (BGMY) CI protein (see AAM34338) that is required for replication. It is
CC encoded by mutated CI open reading frame BGAC190 (see AAT93290). The
CC invention involves production of transgenic plants containing DNA
CC comprising geminivirus CI or AC1 wild-type or mutant sequences that
CC negatively interfere in trans with geminiviral replication during
CC infection. Such transgenic plants are resistant to viral infection. The
CC AC1/CI genes are especially from BGMY, tomato mottle virus or tomato
CC yellow leaf curl virus (see AAT93282-93) and encode polypeptides (see
CC AAM34324-35) that have mutations in the highly conserved DNA-nicking
CC and/or the NTP-binding domains. (Updated on 17-OCT-2003 to standardise OS
CC field)
XX
XX Sequence 353 AA;
SQ
Query Match 81.1%; Score 1572; DB 2; Length 353;
Best Local Similarity 80.4%; Pred. No. 1e-137;
Matches 283; Conservative 31; Mismatches 38; Indels 0; Gaps 0;

Qy      1 MPPPKFRVOSKNYFLTYPOCSLSKEBALSQLQNTLPVKKFKIKIRELHENGEPHLAV 60
Db      1 MPPPKFRVOSKNYFLTYPRCTIPKEEVLSQLQKIHATATNKKFKIVCEBRHENGEPFLHA 60

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[illegible]

RESULT 7
AAW34338
ID AAW34338 standard; protein; 353 AA

DT	17-OCT-2003	(revised)
DT	27-APR-1998	(first entry)

DE Bean golden mosaic geminivirus CI protein.
XX
KM Geminivirus; BGWV; CI gene; transdominant mutation; transgenic plant, disease resistance.

OS Bean golden mosaic virus; type II isolate Guatemala.

PN WO9739110-A1

PD 23-OCT-1997.

PF 15-APR-1997; 97WO-US006300.

PR 16-APR-1996; 96US-0015517P.

PA (SEMI-) SEMINIS VEGETABLE SEEDS INC
10000 WILSON AVENUE
MILWAUKEE, WISCONSIN 53224-1000
TEL: 414/761-1000 FAX: 414/761-1001
WWW: WWW.SEMINIS.COM

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XX
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DR N-PSDB; AAT93314.

PT Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant

PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic

XX
PS Example E: Pass 100-103, English

XX
XX
This document contains the basic control procedures (BCMR) of the project.

transgenic plants containing CI or AC1 wild-type or mutant

CC sequences that negatively interfere in crans with geminiviral replication
CC during infection. Such transgenic plants are resistant to viral

or tomato yellow leaf curl virus (see AY93282-93) and encode infection. The AC1/CI genes are especially from BGWV, comatoc mottle virus

CC conserved DNA-nicking domain and/or the NTP-binding domain (indicated on

17-OCT-2003 to standardise US field

	Query Match	81.1%;	Score 1572;	DB 2;	length 353;
	Best Local Similarity	80.4%;	Pred. No. 137;		
	Matches	283;	Conservative	31;	Mismatches 38; Indels 0; Gaps 0.
Qy	1	MPPPKRRVRSKNTFLTYYPQCSLSKEALSOLQNLNTPVAKKPFKICHELHENGPHLHV			60
Db	1	MPPEQRFRVVSQKNTFLTYPRCPRIKEEVLSQLQIHATNKKFKIKVEERHENGPHLHA			60
Qy	61	LVQEGGYVOCNNNFPLDVSPTFRSAHPHNPQAKSSSDVYSYIDKODGTIEWGFOJIDG			120
Db	61	LIQEGKRFVCTNKLFDLVSTSTRSAHPHNPQAKSSSDVAYAYIDKOSVTIEWGFOYDGS			120
Qy	121	RSARGGQOQSANDSYAKALNAGVSVALAVLREBPCKFVLQNNHRSULERIIPAKAPBPW			180
Db	121	RSARGGQOQSANDSYAKALNADSIISALTITLKEBPCKQVYLQNNHRSULERIIPVAVPEBPW			180
Qy	181	VPPRPGSFNTNVPEMEQEMADNRYEGTGDAAAPDRPVSITIVEGSDRTGTMARALGPHNY			240
Db	181	VPPPLSSFLNIPVVMQEMVDDIYGRGSAARPEPISITIVGDSRTGTMARALGPHNY			240

Qy 301 PAIVLCNPGEGASYKEFLDKAENTGLKNTIKNAFITTLAPLYQESTQASQ 352
|:|||||:|||||:|||||:|||||:|
Db 301 PSIVLCNPGESSYKDFLDKEENRALHNHTIHNAIFVTLAPLYQSTTQDCQ 352

RESULT 8
AAW34333
ID AAW34333 standard; protein; 353 AA

DT	17-OCT-2003	(revised)
DT	27-APR-1998	(first entry)

DE Bean golden mosaic geminivirus C1 BGA221 mutant.

KW Geminiivirus; BGMV; CI gene; transdominant mutation; transgenic plant;

XX

XX

XX

XX

XX XX

XX

PA (WISC) WISCONSIN ALUMNI RES FOUND.

PI Stout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG,

DR WPI; 1997-526447/48.

XX

PT genes - have increased resistance to geminivirus infection e.g. tobacco etch virus

PT *geminivirus*.
xx

Example 5; Page 107-109; 132pp; English

CC This protein comprises a transdominant lethal mutant of the bean golden
CC mosaic virus (BGMV) that is removed for

CC replication. It is encoded by mutated cl open reading frame BGACC221 (see

CC involves production of transgenic plants containing DNA comprising

CC geminivirus CI or AC1 wild-type or mutant sequences that negatively
 CC interfere in trans with geminiviral replication during infection. Such
 CC transgenic plants are resistant to viral infection. The AC1/CI genes are
 CC especially from BGWV, tomato mottle virus or tomato yellow leaf curl
 CC virus (see AAT93282-93) and encode polypeptides (see AAM34324-35) that
 CC have mutations in the highly conserved DNA-nicking and/or the NTP-binding
 CC domains. (Updated on 17-OCT-2003 to standardise OS field)
 CC XX
 SQ Sequence 353 AA;
 Query Match 80.8%; Score 1567; DB 2; Length 353;
 Best Local Similarity 80.1%; Pred. No. 3e-137;
 Matches 282; Conservative 31; Mismatches 39; Indels 0; Gaps 0;
 QY 1 MPPPKRFRVQSKNYFLTYPCQSLSKERALSQLNLNTPVKKFKIKICRELHENGEPHLAV 60
 DB 1 MPPPKRFRVQSKNYFLTYPCQSLSKERALSQLNLNTPVKKFKIKICRELHENGEPHLA 60
 QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSSDVKSYYIDKDGDTIEWGDFQIDG 120
 DB 61 LIQPEGKVCCTNKRFLDLVSTSRAPHPHPIQAKSSSDVKAYIDKDGVTIEWGDFQVDG 120
 QY 121 RSARGGQGSANDSYAKALNAGVOSALAVLREBOPKDFVQNNINIRSNLERIFAKAPEPW 180
 DB 121 RSARGGQGSANDSYAKALNAGVOSALAVLREBOPKDFVQNNINIRSNLERIFAKAPEPW 180
 QY 181 VPPFOVSSFTNVDEMOEMADNYFGTGDAAFPDRPVSIIVEGDSRTGKTMMABALGPHNY 240
 DB 181 VPPFOVSSFTNVDEMOEMADNYFGTGDAAFPDRPVSIIVEGDSRTGKTMMABALGPHNY 240
 QY 241 LSGHLDPNGRVFNVDYQNYVIDIAPHYLKLIKWKELGAKQWQSNCKYKGPVOIKGGI 300
 DB 241 LSGHLDPNGRVFNVDYQNYVIDIAPHYLKLIKWKELGAKQWQSNCKYKGPVOIKGGI 300
 QY 301 PAIVLCNPGGASGYKEFLDKAENTGLKNMTIKKAFITTLTAPLYQSTTQASQ 352
 DB 301 PSLVLCNPGGSSYKDFLDKERNALHNMTIHNAIFVTLTAPLYQSTTQDCQ 352
 RESULT 9
 AAM34334
 ID AAM34334 standard; protein; 353 AA.
 AC AAM34334;
 XX
 XX 17-OCT-2003 (revised)
 DT 27-APR-1998 (first entry)
 DE Bean golden mosaic geminivirus CI BGA228 mutant.
 KM Geminivirus; BGWV; CI gene; transdominant mutation; transgenic plant;
 KM disease resistance.
 OS Bean golden mosaic virus; type II isolate Guatemala.
 OS WO9739110-A1.
 XX
 XX 23-OCT-1997.
 PD
 XX 15-APR-1997; 97WO-US006300.
 PF
 XX 16-APR-1996; 96US-0015517P.
 PR
 XX (SEMT-) SEMINIS VEGETABLE SEEDS INC.
 PA (WISC) WISCONSIN ALUMNI RES FOUND.
 XX
 XX Stout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
 XX WPI: 1997-526447/48.
 DR N-PSDB; AAT93292.
 XX
 PT Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
 PT genes - have increased resistance to geminivirus infection e.g. tomato

PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
 PT geminivirus.
 XX
 XX Example 5; Page 111-112; 132pp; English.
 PS
 XX This protein comprises a transdominant lethal mutant of the bean golden
 CC mosaic virus (BGWV) CI protein (see AAM34338) that is required for
 CC replication. It is encoded by mutated CI open reading frame BGAC228 (see
 CC AAT93292) and carries a mutation in the NTP-binding domain. The invention
 CC involves production of transgenic plants containing DNA comprising
 CC geminivirus CI or AC1 wild-type or mutant sequences that negatively
 CC interfere in trans with geminiviral replication during infection. Such
 CC transgenic plants are resistant to viral infection. The AC1/CI genes are
 CC especially from BGWV, tomato mottle virus or tomato yellow leaf curl
 CC virus (see AAT93282-93) and encode polypeptides (see AAM34324-35) that
 CC have mutations in the highly conserved DNA-nicking and/or the NTP-binding
 CC domains. (Updated on 17-OCT-2003 to standardise OS field)
 CC XX
 SQ Sequence 353 AA;
 Query Match 80.8%; Score 1566; DB 2; Length 353;
 Best Local Similarity 80.1%; Pred. No. 3.7e-137;
 Matches 282; Conservative 31; Mismatches 39; Indels 0; Gaps 0;
 QY 1 MPPPKRFRVQSKNYFLTYPCQSLSKERALSQLNLNTPVKKFKIKICRELHENGEPHLAV 60
 DB 1 MPPPKRFRVQSKNYFLTYPCQSLSKERALSQLNLNTPVKKFKIKICRELHENGEPHLA 60
 QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSSDVKSYYIDKDGDTIEWGDFQIDG 120
 DB 61 LIQPEGKVCCTNKRFLDLVSTSRAPHPHPIQAKSSSDVKAYIDKDGVTIEWGDFQVDG 120
 QY 121 RSARGGQGSANDSYAKALNAGVOSALAVLREBOPKDFVQNNINIRSNLERIFAKAPEPW 180
 DB 121 RSARGGQGSANDSYAKALNAGVOSALAVLREBOPKDFVQNNINIRSNLERIFAKAPEPW 180
 QY 181 VPPFOVSSFTNVDEMOEMADNYFGTGDAAFPDRPVSIIVEGDSRTGKTMMABALGPHNY 240
 DB 181 VPPFOVSSFTNVDEMOEMADNYFGTGDAAFPDRPVSIIVEGDSRTGKTMMABALGPHNY 240
 QY 241 LSGHLDPNGRVFNVDYQNYVIDIAPHYLKLIKWKELGAKQWQSNCKYKGPVOIKGGI 300
 DB 241 LSGHLDPNGRVFNVDYQNYVIDIAPHYLKLIKWKELGAKQWQSNCKYKGPVOIKGGI 300
 QY 301 PAIVLCNPGGASGYKEFLDKAENTGLKNMTIKKAFITTLTAPLYQSTTQASQ 352
 DB 301 PSLVLCNPGGSSYKDFLDKERNALHNMTIHNAIFVTLTAPLYQSTTQDCQ 352
 RESULT 10
 AAM34335
 ID AAM34335 standard; protein; 353 AA.
 AC AAM34335;
 XX
 XX 17-OCT-2003 (revised)
 DT 27-APR-1998 (first entry)
 DE Bean golden mosaic geminivirus CI BGA262 mutant.
 KM Geminivirus; BGWV; CI gene; transdominant mutation; transgenic plant;
 KM disease resistance.
 OS Bean golden mosaic virus; type II isolate Guatemala.
 OS WO9739110-A1.
 XX
 XX 23-OCT-1997.
 PD
 XX 15-APR-1997; 97WO-US006300.
 PF
 XX 16-APR-1996; 96US-0015517P.
 PR
 XX

PA	(SEMI-) SEMINIS VEGETABLE SEEDS INC.
PA	(WISC) WISCONSIN ALUMNI RES FOUND.
PI	Stout JT, Lou HT, Hanson SF, Maxwell DP, Ahlquist PG;
XX	
XX	WP1; 1997-526447/48.
DR	N-PSDB; AAT93293.
XX	
PT	Transgenic plants expressing geminivirus ACI and CI wild-type and mutant
PT	genes - have increased resistance to geminivirus infection e.g. tomato
PT	mottle virus, tomato yellow leaf curl virus or bean golden mosaic
PT	geminivirus.
XX	
PS	Example 5; Page 115-116; 132pp; English.
XX	
CC	This protein comprises a transdominant lethal mutant of the bean golden
CC	mosaic virus (BGV) C1 protein (see AAW34338) that is required for
CC	replication. It is encoded by mutated C1 open reading frame BGAC262 (see
CC	AAT93293) and carries a mutation in the NTP-binding domain. The invention
CC	involves production of transgenic plants containing DNA comprising
CC	geminivirus CI or ACI wild-type or mutant sequences that negatively
CC	interfere in trans with geminiviral replication during infection. Such
CC	transgenic plants are resistant to viral infection. The ACI/C1 genes are
CC	especially from BGV, tomato mottle virus or tomato yellow leaf curl
CC	virus (see AAT93282-93) and encode polypeptides (see AAW34324-35) that
CC	have mutations in the highly conserved DNA-nicking and/or the NTP-binding
CC	domains. (updated on 17-OCT-2003 to standardise OS field)
XX	
SQ	Sequence 353 AA:
Query Match	80.7%; Score 1564; DB 2; Length 353;
Best Local Similarity	80.1%; Pred. No. 5.7e-137;
Matches 282; Conservative 31; Mismatches 39; Indels 0; Gaps 0;	
DQ	1 MPPEKKPFVOSKNFLTYPOCSLSKEALISOLUNLTVNKKFICRCEIHNGEPHIV 60 : : : : 1 MPPEKRFVOSKNFLTYPCIPKEEVLSQLCKHTTKNKFKIVCERHNGEPHLHA 60
Db	
DQ	61 LVPEGKYQCTNNNEFDLVSPETRSARHPNTIQGAKSSSDVYSIDKDGTITMGDFQIDG 120 : : : : 61 LIPEGKRVCTNKKLFDLVSSTRSAPRPNPQGAKSSSDVAYIXDGGVTITMGDFQYDG 120
Db	
DQ	121 RSAAGGQGSANDSYAKALNAGSVGALAVALAEQPKDYVLQNHNTRSLERIFAAAPBPW 180 : : : : 121 RSAAGGQGSANDSYAKALNAGSIIESALTILKEEQPKDYVLQHNRNSLERIFAVPBPW 180
Db	
DQ	181 VPPEVSSFTVPBEMOEMADNYFCGTGAAPDRVSTIIIEGDSRTGKTMMRALGPNNY 240 : : : : 181 VPPEPLSSFNVPPVMQEMVDYDFRGSAARPERISIIIEGDSRTGKTMMRALGPNNY 240
Db	
DQ	241 LSGHLDENGRAVFSNDVQYNVIDIAAPHYLKLGMKELLGAOKDMQSNCKYGRPVQIKGI 300 : : : : 241 LSGHLDENSRVYNAVEYNVIRDISPNYLKLGMKELIGAQDMQSNCKYGRPVQIKGI 300
Db	
DQ	301 PATVLCNPGEGASYPELPDKAENGLKMKWTIKNAFILTLTAPLYGESYQAQ 352 : : : : 301 PSIVLCNPGEGSYKDFDKENRALHNMVTHNALFVLTAPLYOSTTQDCQ 352
Db	
RESULT 11	
AAAB16687	standard; peptide; 356 AA.
XX	
XX	AAAB16687;
DE	22-JAN-2001 (first entry)
XX	
XX	Amino acid sequence of a geminivirus replication protein of TGWV.
KM	Geminivirus; replication protein; Rep protein; AL1; transgenic plant;
KW	ribosome binding region; resistance; geminivirus infection.
XS	Tomato golden mosaic virus.

[illegible]

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ID AAR8872 standard; protein; 359 AA.
XX
AC AAR8872;
XX
DT 27-AUG-2003 (revised)
DT 07-NOV-1996 (first entry)
XX
DE Sardinian tomato yellow leaf curl virus mutated Rep protein (K227R).
XX
KM Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
KM modification; mutation; viral replication; deficient; inhibition;
KM viral resistance; geminivirus; tomato yellow leaf curl virus;
KM Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 protein;
KM A11 protein.
XX
OS Tomato yellow leaf curl virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 227
FT /note= "wild-type Lys has been replaced by Arg"
XX
PN WO9608573-A1.
XX
PD 21-MAR-1996.
XX
PF 15-SEP-1995; 95WO-FR001192.
XX
PR 15-SEP-1994; 94FR-00011040.
XX
PA (CNRS ) CENT NAT RECH SCI.
XX
PI Gronenborn B;
XX
DR WPI; 1996-179947/18.
XX
DR N-PSDB; AAT12906.
XX
PT Prod. of virus-resistant transgenic plants - using mutated genomic
PT sequence from phytopathogenic DNA virus.
XX
PS Disclosure; Fig 13; 93pp; French.
XX
CC Mutation of consensus amino acids in the NTP-binding site of geminivirus
CC Rep protein is used to produce replication deficient viruses. The mutated
CC viral nucleic acid is used for producing transgenic plants that are
CC resistant to, or tolerant of, the native virus. The present sequence is a
CC mutant form of the Rep (or C1) protein from the Sardinian isolate of
CC tomato yellow leaf curl virus (STYLCV) in which the wild-type Lys227
CC residue has been changed to an Arg residue; transgenic Nicotiana
CC benthamiana plants generated by transformation with the mutated virus
CC were not resistant to STYLCV. In contrast, plants transformed with a
CC virus in which Lys227 had been replaced by Ala were found to be
CC resistant. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 359 AA;
XX
Query Match 67.5%; Score 1308.5; DB 2; Length 359;
Best Local Similarity 66.0%; Pred. No. 4.2e-113;
Matches 239; Conservative 49; Mismatches 65; Indels 9; Gaps 4;
QY 1 MPPPKKRRVQSKNYFLTYPOCSLSKEBALSQLONTLPVKKFKIKICREIHENGEPIHAY 60
DB 1 MPPSGRFSIAKKNVFLTYPKCDLTKENALSGITVLQTFPNKLFIKICREIHENGEPIHAI 60
QY 61 LVQFEGKYOCNTNRFPLVSPTRSAHFHPNIQKSSDVKSYIDKQDGTIEWDFOIDG 120
DB 61 LIFQEGKYNTCNQFPLVSPTRSAHFHPNIQKSSDVKSYIDKQDVLIEWGTFOIDG 120
QY 121 RSARGGQGSANDSYAKALNNGSVQALAVLEEQKDFVLONHNRISNLERIFAKAPEPW 180
DB 121 RSARGGQGTANDAAKAINNGSKQALDVIKELAPRIVLHFNHINSLDKVFPVPAFY 180
QY 181 VPPFQVSSFTNVPEDEQEW-ADNYFGTGDAAPDPDPVSIIVEGDSRTGKTMARALGPHN 239

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DB 181 VSPFLSSFPQVPEDELEHWSENVMDA--AAPRPRVSIIVEGDSRTGRTTWARSLGPHN 238
QY 240 YLSGHLDPNGRVPSNDVQVNVVIDDIAPHYKLGKMKELLGAQDWMQNCYGVQIKG 299
DB 239 YLGHLDLSQKYSNNAMVVIDVDPHY--LGHFKSEMGARQDWMQNTYKPIQIKG 296
QY 300 IPAIVLCNPEGASKEYEFLDKAENTGKNTIKNAIFITLTAPLY-----QESTQASQETG 355
DB 297 IPIIFLCNPPQSSFKYLDDEKNQALKMATNAIVTTHQPLFADTQNTISHRQEA 356
QY 356 NQ 357
DB 357 SR 358
XX
RESULT 13
ID AAR8871 standard; protein; 359 AA.
XX
AC AAR8871;
XX
DT 27-AUG-2003 (revised)
DT 07-NOV-1996 (first entry)
XX
DE Sardinian tomato yellow leaf curl virus mutated Rep protein (K227H).
XX
KM Nucleotide triphosphate binding site; DNA helicase; RNA helicase;
KM modification; mutation; viral replication; deficient; inhibition;
KM viral resistance; geminivirus; tomato yellow leaf curl virus;
KM Sardinian isolate; STYLCV; transgenic plant; P-loop; C1 protein;
KM A11 protein.
XX
OS Tomato yellow leaf curl virus.
XX
FH Key Location/Qualifiers
FT Misc-difference 227
FT /note= "wild-type Lys has been replaced by His"
XX
PN WO9608573-A1.
XX
PD 21-MAR-1996.
XX
PF 15-SEP-1995; 95WO-FR001192.
XX
PR 15-SEP-1994; 94FR-00011040.
XX
PA (CNRS ) CENT NAT RECH SCI.
XX
PI Gronenborn B;
XX
DR WPI; 1996-179947/18.
XX
DR N-PSDB; AAT12905.
XX
PT Prod. of virus-resistant transgenic plants - using mutated genomic
PT sequence from phytopathogenic DNA virus.
XX
PS Disclosure; Fig 13; 93pp; French.
XX
CC Mutation of consensus amino acids in the NTP-binding site of geminivirus
CC Rep protein is used to produce replication deficient viruses. The mutated
CC viral nucleic acid is used for producing transgenic plants that are
CC resistant to, or tolerant of, the native virus. The present sequence is a
CC mutant form of the Rep (or C1) protein from the Sardinian isolate of
CC tomato yellow leaf curl virus (STYLCV) in which the wild-type Lys227
CC residue has been changed to a His residue; transgenic Nicotiana
CC benthamiana plants generated by transformation with the mutated virus
CC were not resistant to STYLCV. In contrast, plants transformed with a
CC virus in which Lys227 had been replaced by Ala were found to be
CC resistant. (Updated on 27-AUG-2003 to correct OS field.)
XX
SQ Sequence 359 AA;
XX
Query Match 67.3%; Score 1305.5; DB 2; Length 359;

```

	Best Local Similarity	66.0%	Pred. No. 8e-113;	
Matches	239;	Conservative	48;	Mismatches 66; Indels 9; Gaps 4
QY	1	MPPKKRFRVQSKNYFLITYPOCSLSKEEALSQLONINTPVNKKFIKICREIHENGEPHLIV	60	
		1	MPRGRGFRFIKAKNYFLITYPKCDLTKENALSLQITINLOTFTNKLFIKICREIHENGEPHLIH	60
QY	61	LVQREBKQKQCTNNRREFDLVSPTRSHAFHPNIOGAASSSDVSYIDKOGDTIEMGFOJIDG	120	
		61	LIQREBKKNCTNORFFDLVSPTRSHAFHPNIOGAASSSDVSYIDKOGDVLWEGTFOJIDG	120
QY	121	RSAGGQGSANDSVYKALNAGSVQSAALVLRREOKPDFVLQWHTNRSLNERIFALAPBPW	180	
		121	RSAGGQGTANDAYAKALNAGSKGALDVYIKELAPRDVYLHPHNTNSINDKVFQVPPAPAY	180
QY	181	VPPEOVSSFTVWPDEMOEW-ADNYEGTGDAAPDRPVSIIVEGDSRTGKTMMARALGPHN	239	
		181	VSPFLSSFFDQVPDELEHWSBNWDA--AAPRPMKPVSIIVEGDSRTGHTTWARSLGPHN	238
QY	240	YLSGHLDFNGRVSNDVOYNNVIDIAPHYLKIKHKMKELLAGQKDNQSNCKTGKPVQIKGG	299	
		239	YLCGHLDFSQKYSNNAMVNNVIDVDVPHY--LKHFKEFWGAQRDQSNTRYKGPQIKGG	296
QY	300	IPALVLCNRPBGASVKEFLDKRAENTGLKWTITKNAIFITLTPLVX----QESTQASQETG	355	
		297	IPITFLCNRPQSSPEKYEIDEEKQALKNWATKNAIFVTHIQPLPADTNQNTTSHROEBA	356
QY	356	NO 357		
		357	SE 358	

Accession	Protein	Gene	Organism	Accession	Protein	Gene	Organism
AA088870	standard; protein; 359 AA.			AA088870	standard; protein; 359 AA.		
AA088870				AA088870			
27-AUG-2003	(revised)			27-AUG-2003	(revised)		
07-NOV-1996	(first entry)			07-NOV-1996	(first entry)		
Sardinian tomato	yellow leaf curl virus mutated Rep protein (K227A)			Sardinian tomato	yellow leaf curl virus mutated Rep protein (K227A)		
Nucleotide triphosphate binding site; DNA helicase; RNA helicase; modification; mutation; viral replication; deficiency; inhibition; viral resistance; geminivirus; tomato yellow leaf curl virus; Sardinian isolate; STYLVC; transgenic plant; P-loop; C1 protein; A11 protein; dominant negative phenotype.				Nucleotide triphosphate binding site; DNA helicase; RNA helicase; modification; mutation; viral replication; deficiency; inhibition; viral resistance; geminivirus; tomato yellow leaf curl virus; Sardinian isolate; STYLVC; transgenic plant; P-loop; C1 protein; A11 protein; dominant negative phenotype.			
Tomato yellow leaf curl virus.				Tomato yellow leaf curl virus.			
Key	Location/Qualifiers			Key	Location/Qualifiers		
Misc-difference 227	/note= "wild-type Lys has been replaced by Ala"			Misc-difference 227	/note= "wild-type Lys has been replaced by Ala"		
MO9608573-A1.				MO9608573-A1.			
21-MAR-1996.				21-MAR-1996.			
15-SEP-1995;	95WO-FR001192.			15-SEP-1995;	95WO-FR001192.		
15-SEP-1994;	94PR-00011040.			15-SEP-1994;	94PR-00011040.		
(CNRS)	CENT NAT RECH SCT.			(CNRS)	CENT NAT RECH SCT.		
Gronenborn B;				Gronenborn B;			
WPI; 1996-179947/18.				WPI; 1996-179947/18.			
N-PSDB; AAT12904.				N-PSDB; AAT12904.			
Prodn. of virus-resistant transgenic plants - using mutated genomic sequence from phytopathogenic DNA virus.				Prodn. of virus-resistant transgenic plants - using mutated genomic sequence from phytopathogenic DNA virus.			

PS Disclosure; Fig 13; 93pp; French.
XX
CC Mutation of consensus amino acids in the NTP-binding site of geminivirus
CC Rep protein is used to produce replication deficient viruses. The mutated
CC viral nucleic acid is used for producing transgenic plants that are
CC resistant to, or tolerant of, the native virus. The present sequence is a
CC mutant form of the Rep (or CI) protein from the Sardinian isolate of
CC tomato yellow leaf curl virus (STYLVCV) in which the wild-type 1ys827
CC residue has been changed to an Ala residue; transgenic Nicotiana
CC benthamiana plants generated by transformation with the mutated virus
CC were found to be resistant to STYLVCV, i.e. the mutation results in a
CC dominant negative phenotype. (Updated on 27-AUG-2003 to correct OS
CC field.)
XX
SQ Sequence 359 AA;

Query Match	Similarity	67.3%	Score 1305.5	DB 2	Length 359
Best Local	Similarity	66.0%	Pred. No. 8e-113		
Matches	239	Conservative	48	Mismatches	66
				Indels	9
				Gaps	4
Qy	1	MPPKKRFRVOSKNYFLTYPOCSKEBALSOLONLNTPVNNKFLIKICREIHENGPHLHV	60		
		1	MPRGSRFISAKNKNFLTYPKCDLTKEKALISQITNLQPTPNKLFIKICREIHENGPHLHI	60	
Db					
Qy	61	LVOPEGKYOCNNRFFPLVSPPTBSAHHHPNIQAKSSSDVSYIDKOGDTEWGPFOIDG	120		
		61	LIOEGKKNCTNOFFPLVSPPTBSAHHHPNIQAKSSSDVSYIDKOGDTEWGPFOIDG	120	
Db					
Qy	121	RSARGQOQASNDASYAKALNAGSVOSALAVLREBPQKPFVLONHNIRSNLERIFAKAPEPW	180		
		121	RSARGQGTANDAVAKALNAGSKQALDVIKELAPRYVYLHFHNINSRLDKVFQPPAPFY	180	
Db					
Qy	181	VPPPVQSSFTNVPEEMQEW-ADNTFGTGDAAPRP RPSPSIIYEGSRCTKTMARALGPHN	239		
		181	VSPLSSFPQVDPBELHFWSENMDA--AARPMRPVSIVYEGSRCTGATTMARSLGPHN	238	
Db					
Qy	240	YLGSGLHPNGRVFENDVQVYNYIDIIAPHYLKIKMKKELLGAKQKQMSNCKTKGKPVQIKGG	299		
		239	YLCHLHDSQKRVYSNNAMTYNVIDVDPHY--LKFIFKEMGQRQWQSTTKGKPIQIKGG	296	
Db					
Qy	300	IPALVLCNPEGASKEYELDKAENTGLKNWTTIKNAIFITTLAPLY---QESTQASQETG	355		
		297	IPFLFLCNPGQSSFKREYLDSEKQALKNATKNAIFVITIHQPLPADTNQWTTSHROEA	356	
Db					
Qy	356	NQ 357			
		::			
Db		357	SE 358		

	RESULT	15
XX	AAW34337	
XX	AAW34337	standard; protein; 357 AA.
XX	AAW34337;	
XX	17-OCT-2003	(revised)
XX	27-APR-1998	(first entry)
XX	Tomato yellow leaf curl virus CI protein.	
XX	Geminivirus; TYLCV; CI gene; transdominant mutation; transgenic plant.	
XX	disease resistance.	
XX	Tomato yellow leaf curl virus; strain Israel.	
XX	WO9739110-A1.	
XX	23-OCT-1997.	
XX	15-APR-1997;	97WO-US006300.
XX	16-APR-1996;	96US-0015517P.

PA (SEMI-) SEMINIS VEGETABLE SEEDS INC.
PA (MISC) WISCONSIN ALUMNI RES FOUND.

XX Stout JT, Luu HT, Hanson SF, Maxwell DP, Ahlquist PG;
XX WPI; 1997-526447/48.

XX DR N-PSDB; AAT93311.

XX Transgenic plants expressing geminivirus AC1 and CI wild-type and mutant
PT genes - have increased resistance to geminivirus infection e.g. tomato
PT mottle virus, tomato yellow leaf curl virus or bean golden mosaic
PT geminivirus.

XX Example 4.1; Page 80-81; 132pp; English.

CC This protein comprises the wild-type CI protein of tomato yellow leaf
CC curl virus (TYLCV), a geminivirus that has a monopartite genome. The CI
CC protein is required for replication. The invention involves production of
CC transgenic plants containing DNA comprising geminivirus AC1 or CI wild-
CC type or mutant sequences that negatively interfere in trans with
CC geminiviral replication during infection. Such transgenic plants are
CC resistant to viral infection. The AC1/CI genes are especially from TYLCV,
CC tomato mottle virus or bean golden mosaic geminivirus (see AAT93282-93)
CC and encode polypeptides (see AAW34324-35) that can have mutations in the
CC highly conserved DNA-nicking domain and/or the NTP-binding domain.
CC (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 357 AA;

Query Match 66.7%; Score 1293.5; DB 2; Length 357;

Best Local Similarity 66.3%; Pred. No. 1e-111;
Matches 238; Conservative 53; Mismatches 59; Indels 9; Gaps 4;

QY 4 PKKRVQSKNYFLTYPCQSLSKERALSOLOLNTLPVKKFKICRELHENGEPHLAVLYQ 63
DB 2 PLRFKITYAKNFFLYPCSLSKERALSOQLKLETPNKKYIKVCKELHENGEPHLAVLIQ 61
QY 64 FEGKYQCTNNRFFDLVSPTRSAHFHPNIQCAKSSDVSYIDKDDTIEWGDFQIDGRSA 123
DB 62 FEGKYQCKNGRFFDLVSPNRSAHFHPNIQAKSSTDVKTVEKDNFIDFGVSQIDGRSA 121
QY 124 RGGQOSANDSYAKALANGSVOSALAVREBOPKDFVLQNNHINIRSNLERIFAKAPEPVPP 183
DB 122 RGGQOSANDYAEALNGSISEALNIIKEKAPKDYIIQFHNLSNLDRIFFSPPEVYVSP 181
QY 184 FOVSFFTNVDEMEW-ADNYFGTGDAPPRPVSIIVEGDSRTGKTMARALGPHNYIS 242
DB 182 FLSSSFNQVPEDELEWVAENV-VYSAPRPWPPISTIVIEGDSRTGKTMARSLGPHNYLC 239
QY 243 GHLDENGRVFSNDVQYVVIDIAPHYLKLKMKELLAGOKDMQSNCKYKRPVQIKGIPPA 302
DB 240 GHLDLSPKYSNDAMWYVIDVNPY--LKHFKFIMAQRDMQSNCKYKRPVQIKGIPPT 297
QY 303 IVLGNPEGASYSKFFLDKAENTGLKNTTIKNAFITTLAPLY---QESTQASQETGNQ 357
DB 298 IFLCNPGPTSSYRREYDEKKNISLKNWALKNATFTVLYEPFASINQPTQDSQETNKK 356

Search completed: December 3, 2004, 14:57:29
Job time: 159 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2004, 14:58:24 ; Search time 22 Seconds
(without alignments)
1088.218 Million cell updates/sec

Title: US-09-491-063a-2

Perfect score: 1939
Sequence: 1 MPPPKKFRVQSKNYFLTYPO.....PLYQSTQASQETGNKAGG 361

Scoring table: BLOSUM62
Gapcp 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/prodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/prodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/prodata/1/iaa/PCITUS_COMB.pep:*
6: /cgn2_6/prodata/1/iaa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1908	98.4	361	3	US-08-838-151A-2
2	1902	98.1	361	3	US-08-838-151A-6
3	1892	97.6	361	3	US-08-838-151A-8
4	1886	97.3	361	3	US-08-838-151A-4
5	1572	81.1	353	3	US-08-838-151A-44
6	1572	81.1	353	3	US-08-838-151A-46
7	1567	80.8	353	3	US-08-838-151A-49
8	1566	80.8	353	3	US-08-838-151A-52
9	1564	80.7	353	3	US-08-838-151A-55
10	1311.5	67.6	359	3	US-08-809-103B-2
11	1308.5	67.5	359	3	US-08-809-103B-8
12	1305.5	67.3	359	3	US-08-809-103B-4
13	1305.5	66.7	359	3	US-08-809-103B-6
14	1293.5	66.7	357	3	US-08-838-151A-20
15	1293.5	66.7	357	3	US-08-838-151A-24
16	1290.5	66.6	357	3	US-08-838-151A-27
17	1288.5	66.5	357	3	US-08-838-151A-30
18	1288.5	66.1	357	3	US-08-838-151A-14
19	486	25.1	335	3	US-09-414-276-6
20	275.5	14.2	293	3	US-09-414-276-3
21	241	12.4	133	3	US-09-414-276-4
22	141	7.3	27	2	US-08-967-999-4
23	141	7.3	27	2	US-08-967-999-5
24	113	5.8	472	2	US-08-811-949-63
25	108	5.6	27	2	US-08-967-999-6
26	108	5.6	27	2	US-08-967-999-7
27	103.5	5.3	527	4	US-09-600-985-1

28	103.5	5.3	527	4	US-09-600-985-2	Sequence 2, Appl
29	103.5	5.3	527	4	US-09-600-985-3	Sequence 3, Appl
30	102.5	5.3	437	2	US-08-811-949-49	Sequence 49, Appl
31	102.5	5.3	527	1	US-07-609-510B-16	Sequence 16, Appl
32	102.5	5.3	527	4	US-09-612-314A-51	Sequence 51, Appl
33	102.5	5.3	527	5	PCT-US91-01025A-2	Sequence 2, Appl
34	102.5	5.3	527	6	5185259-8	Patent No. 5185259
35	102.5	5.3	562	2	US-08-811-949-43	Sequence 43, Appl
36	102.5	5.3	562	2	US-08-560-098A-50	Sequence 50, Appl
37	102.5	5.3	562	2	US-08-883-795A-38	Sequence 38, Appl
38	102.5	5.3	562	4	US-09-703-695A-4	Sequence 4, Appl
39	102.5	5.3	562	6	5185259-3	Patent No. 5185259
40	102.5	5.3	562	6	5200340-2	Patent No. 5200340
41	102.5	5.3	562	6	5344773-2	Patent No. 5344773
42	101.5	5.2	437	2	US-08-811-949-55	Sequence 55, Appl
43	101.5	5.2	527	6	5520913-1	Patent No. 5520913
44	97	5.0	671	4	US-09-543-681A-5122	Sequence 5122, Ap
45	96	5.0	263	4	US-09-248-796A-23610	Sequence 23610, A

ALIGNMENTS

```
RESULT 1
US-08-838-151A-2
Sequence 2, Application US/0838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Lau, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Gemminivirus
NUMBER OF INVENTIONS: 1
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSER: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
US-08-838-151A-2
Query Match 98.4%; Score 1908; DB 3; Length 361;
Best Local Similarity 98.3%; Pred. No. 2,5e-189;
Matches 355; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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Db 1 MPPPKKRRVQSKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKIKCRELHENGEPHLHV 60
QY 61 LVQPEGKYQCTNNRFFDLVSPTRSAHFHPNIQAKSSSDVKSYYDKQDITTEMGDFOIDG 120
Db 61 LVQPEGKYQCTNNRFFDLVSPTRSAHFHPNIQAKSSSDVKSYYDKQDITTEMGDFOIDG 120
QY 121 RSARGGQGSANDSYAKALNAGSVQSAIAVIREOPKDFVLQNNHNRSLERIFAKABEPW 180
Db 121 RSARGGQGSANDSYAKALNAGSVQSAIAVIREOPKDFVLQNNHNRSLERIFAKABEPW 180
QY 181 VPPQVSSFTNVDPMEQEMADNFGTGDAAAPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
Db 181 VPPQVSSFTNVDPMEQEMADNFGTGDAAAPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
QY 241 LSGHLDNGRVSNDVQYNYIDIAPHYLLKTKMKELGAKQKQMSCKTGKPVQIRGGI 300
Db 241 LSGHLDNGRVSNDVQYNYIDIAPHYLLKTKMKELGAKQKQMSCKTGKPVQIRGGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTKKNAIFITLTAPLYQDSTQASQETGNOQAK 360
Db 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTKKNAIFITLTAPLYQDSTQASQETGNOQAK 360
QY 361 G 361
Db 361 G 361

RESULT 2

US-08-838-151A-6
Sequence 6, Application US/08838151A
Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838.151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-6

Query Match 98.1%; Score 1902; DB 3; Length 361;
Best Local Similarity 98.1%; Pred. No. 1e-188;

Matches 354; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 MPPPKKRRVQSKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKIKCRELHENGEPHLHV 60
Db 1 MPPPKKRRVQSKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKIKCRELHENGEPHLHV 60
QY 61 LVQPEGKYQCTNNRFFDLVSPTRSAHFHPNIQAKSSSDVKSYYDKQDITTEMGDFOIDG 120
Db 61 LVQPEGKYQCTNNRFFDLVSPTRSAHFHPNIQAKSSSDVKSYYDKQDITTEMGDFOIDG 120
QY 121 RSARGGQGSANDSYAKALNAGSVQSAIAVIREOPKDFVLQNNHNRSLERIFAKABEPW 180
Db 121 RSARGGQGSANDSYAKALNAGSVQSAIAVIREOPKDFVLQNNHNRSLERIFAKABEPW 180
QY 181 VPPQVSSFTNVDPMEQEMADNFGTGDAAAPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
Db 181 VPPQVSSFTNVDPMEQEMADNFGTGDAAAPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
QY 241 LSGHLDNGRVSNDVQYNYIDIAPHYLLKTKMKELGAKQKQMSCKTGKPVQIRGGI 300
Db 241 LSGHLDNGRVSNDVQYNYIDIAPHYLLKTKMKELGAKQKQMSCKTGKPVQIRGGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTKKNAIFITLTAPLYQDSTQASQETGNOQAK 360
Db 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTKKNAIFITLTAPLYQDSTQASQETGNOQAK 360
QY 361 G 361
Db 361 G 361

RESULT 3

US-08-838-151A-8
Sequence 8, Application US/08838151A
Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838.151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-838-151A-8

Query Match 97.6%; Score 1892; DB 3; Length 361;
Best Local Similarity 97.8%; Pred. No. 1.1e-187;
Matches 353; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 MPPPKRRVSKYFLTYPCSSLSKEALSQLNLNTPVNKKFKIKICREHENGEPHLAV 60
DB 1 MPPPKRRVSKYFLTYPCSSLSKEALSQLNLNTPVNKKFKIKICREHENGEPHLAV 60
QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSSDVKSYYIDKGDITTEMGDFQIDG 120
DB 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSSDVKSYYIDKGDITTEMGDFQIDG 120
QY 121 RSARGGQOSANDSYAKALNAGSVQALAVLREOPKDFVLQNNHINSNLERIFAKAPEPW 180
DB 121 RSARGGQOSANDSYAKALNAGSVQALAVLREOPKDFVLQNNHINSNLERIFAKAPEPW 180
QY 181 VPPFOVSSFTNVPEDEMEADNYFGTGAAPPRPVSIIVEGDSRTGKTMMARALGPHNY 240
DB 181 VPPFOVSSFTNVPEDEMEADNYFGTGAAPPRPVSIIVEGDSRTGKTMMARALGPHNY 240
QY 241 LSGHLDNNGRVFSDVQYNYVIDIAPHYLKIKMKELLAGQKQKQMSCKTGKPVQIKGI 300
DB 241 LSGHLDNNGRVFSDVQYNYVIDIAPHYLKIKMKELLAGQKQKQMSCKTGKPVQIKGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTYKNAIFITTLTAPLYQDSTQASQETGNQKQ 360
DB 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTYKNAIFITTLTAPLYQDSTQASQETGNQKQ 360
QY 361 G 361
DB 361 G 361

RESULT 4

US-08-838-151A-4
Sequence 4, Application US/08838151A

Patent No. 6291743
GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Luu, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus

TITLE OF INVENTION: Genes

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Rocky, Milnamow & Katz

STREET: Two Prudential Plaza, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,151A

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SVS3801P0260

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:

LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-4

Query Match 97.3%; Score 1886; DB 3; Length 361;
Best Local Similarity 97.5%; Pred. No. 4.7e-187;
Matches 352; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MPPPKRRVSKYFLTYPCSSLSKEALSQLNLNTPVNKKFKIKICREHENGEPHLAV 60
DB 1 MPPPKRRVSKYFLTYPCSSLSKEALSQLNLNTPVNKKFKIKICREHENGEPHLAV 60
QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSSDVKSYYIDKGDITTEMGDFQIDG 120
DB 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSSDVKSYYIDKGDITTEMGDFQIDG 120
QY 121 RSARGGQOSANDSYAKALNAGSVQALAVLREOPKDFVLQNNHINSNLERIFAKAPEPW 180
DB 121 RSARGGQOSANDSYAKALNAGSVQALAVLREOPKDFVLQNNHINSNLERIFAKAPEPW 180
QY 181 VPPFOVSSFTNVPEDEMEADNYFGTGAAPPRPVSIIVEGDSRTGKTMMARALGPHNY 240
DB 181 VPPFOVSSFTNVPEDEMEADNYFGTGAAPPRPVSIIVEGDSRTGKTMMARALGPHNY 240
QY 241 LSGHLDNNGRVFSDVQYNYVIDIAPHYLKIKMKELLAGQKQKQMSCKTGKPVQIKGI 300
DB 241 LSGHLDNNGRVFSDVQYNYVIDIAPHYLKIKMKELLAGQKQKQMSCKTGKPVQIKGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTYKNAIFITTLTAPLYQDSTQASQETGNQKQ 360
DB 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTYKNAIFITTLTAPLYQDSTQASQETGNQKQ 360
QY 361 G 361
DB 361 G 361

RESULT 5

US-08-838-151A-44
Sequence 44, Application US/08838151A

Patent No. 6291743

GENERAL INFORMATION:

APPLICANT: Stout, John T

APPLICANT: Luu, Hang T

APPLICANT: Maxwell, Douglas

APPLICANT: Ahlquist, Paul

TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus

TITLE OF INVENTION: Genes

NUMBER OF SEQUENCES: 63

CORRESPONDENCE ADDRESS:

ADDRESSEE: Dressler, Rocky, Milnamow & Katz

STREET: Two Prudential Plaza, Suite 4700

CITY: Chicago

STATE: Illinois

COUNTRY: U.S.A.

ZIP: 60601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/838,151A

FILING DATE:

CLASSIFICATION: 800

ATTORNEY/AGENT INFORMATION:

NAME: Mueller, Lisa V

REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SVS3801P0260

TELEPHONE: 312-616-5400

TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 44:

SEQUENCE CHARACTERISTICS:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-44

Query Match 81.1%; Score 1572; DB 3; Length 353;
Best Local Similarity 80.4%; Pred. No. 1.8e-154;
Matches 283; Conservative 31; Mismatches 38; Indels 0; Gaps 0;

QY 1 MPPPKRRVSKNYFLTYPCQSLSKERALSQLQNLNPNVKKFKIKRELHENGEPHLAV 60
DB 1 MPPQRRVRSKNVFLTYPCPIPKKEVLSQLQKHATNKKFKVCEERHENGEPHLA 60
QY 61 LVPEGRKYQCTNNRFPDLVSPTRSAHPHNPNOGAKSSSDVKSXIDKDGDTIEMGDFQIDG 120
DB 61 LIQPEGKFCVCTNKRFLPLVSTSRAPHPNPNOGAKSSSDVKAVIDKDGVTIEMGDFQVDS 120
QY 121 RSARGGQGSANDSYAKALNAGVQSLAVLREOPKDFVLQNNHNSNLERIFAKADEPW 180
DB 121 RSARGGQGSANDSYAKALNADSIRESALTILKEQPKDYVLQHHNIRSNLERIFVKYDEPW 180
QY 181 VPPQVSSFTNVDEMOMADNYFGTGDAPRDRPVSIYEGDSRTGKTMMARALGPHNY 240
DB 181 VPPPLSSFTNVPMQEWDDYFGRSAPRPERPISIIYEGDSRTGKTMMARALGPHNY 240
QY 241 LSGHLDNFGVFSNDVQYNNVIDIAPHYLKLKMKKELGAKQKQMSCKYKGPVQIKGI 300
DB 241 LSGHLDNFSNVNAVYNNVIDISPYLKLKMKKELGAKQKQMSCKYKGPVQIKGI 300
QY 301 PAIVLCNPGGASYSKEFLDKAENTGLKNWTKNAIFITLTPALPYQSTQASQ 352
DB 301 PSIVLCNPGGSSYKDFLDKEENRALHNTIHNAIFVTLTPALPYQSTTQDCQ 352

RESULT 6
US-08-838-151A-46
Sequence 46, Application US/08838151A
Patent No. 6291743

GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-46

Query Match 81.1%; Score 1572; DB 3; Length 353;
Best Local Similarity 80.4%; Pred. No. 1.8e-154;
Matches 283; Conservative 31; Mismatches 38; Indels 0; Gaps 0;

QY 1 MPPPKRRVSKNYFLTYPCQSLSKERALSQLQNLNPNVKKFKIKRELHENGEPHLAV 60
DB 1 MPPQRRVRSKNVFLTYPCPIPKKEVLSQLQKHATNKKFKVCEERHENGEPHLA 60
QY 61 LVPEGRKYQCTNNRFPDLVSPTRSAHPHNPNOGAKSSSDVKSXIDKDGDTIEMGDFQIDG 120
DB 61 LIQPEGKFCVCTNKRFLPLVSTSRAPHPNPNOGAKSSSDVKAVIDKDGVTIEMGDFQVDS 120
QY 121 RSARGGQGSANDSYAKALNAGVQSLAVLREOPKDFVLQNNHNSNLERIFAKADEPW 180
DB 121 RSARGGQGSANDSYAKALNADSIRESALTILKEQPKDYVLQHHNIRSNLERIFVKYDEPW 180
QY 181 VPPQVSSFTNVDEMOMADNYFGTGDAPRDRPVSIYEGDSRTGKTMMARALGPHNY 240
DB 181 VPPPLSSFTNVPMQEWDDYFGRSAPRPERPISIIYEGDSRTGKTMMARALGPHNY 240
QY 241 LSGHLDNFGVFSNDVQYNNVIDIAPHYLKLKMKKELGAKQKQMSCKYKGPVQIKGI 300
DB 241 LSGHLDNFSNVNAVYNNVIDISPYLKLKMKKELGAKQKQMSCKYKGPVQIKGI 300
QY 301 PAIVLCNPGGASYSKEFLDKAENTGLKNWTKNAIFITLTPALPYQSTQASQ 352
DB 301 PSIVLCNPGGSSYKDFLDKEENRALHNTIHNAIFVTLTPALPYQSTTQDCQ 352

RESULT 7
US-08-838-151A-49
Sequence 49, Application US/08838151A
Patent No. 6291743

GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-49

Query Match 80.8%; Score 1567; DB 3; Length 353;
Best Local Similarity 80.1%; Pred. No. 6e-154;
Matches 282; Conservative 31; Mismatches 39; Indels 0; Gaps 0;

QY 1 MPPPKFRVQSKNYFLTYPCQSLSKERALSQLQNLTPVNNKFKIKICREIHENGEPHLAV 60
DB 1 MPPPKFRVQSKNYFLTYPCQSLSKERALSQLQNLTPVNNKFKIKICREIHENGEPHLAV 60
QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDYKSYIDKDGDTIEMGDFOIDG 120
DB 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDYKSYIDKDGDTIEMGDFOIDG 120
QY 121 RSARGGQOSANDSYAKALNAGVOSALAVAREOPKDFVLQNHINIRSNLERIFAKAPEPW 180
DB 121 RSARGGQOSANDSYAKALNAGVOSALAVAREOPKDFVLQNHINIRSNLERIFAKAPEPW 180
QY 181 VPPFOVSSFTNVDEMOMADNYFGTDAAPPRPVSIIVEGDSRTGKTWABALGPHNY 240
DB 181 VPPFOVSSFTNVDEMOMADNYFGTDAAPPRPVSIIVEGDSRTGKTWABALGPHNY 240
QY 241 LSGHLDPNHGVFNVDQVNYIDIAPIHYLKLKMKWELGAKQWQSNCKYKGPVQIKGI 300
DB 241 LSGHLDPNHGVFNVDQVNYIDIAPIHYLKLKMKWELGAKQWQSNCKYKGPVQIKGI 300
QY 301 PATVLCNPGSGASYKEFLDKAENTGLKNMTIKVAIFITLTAPLYOSTQASQ 352
DB 301 PATVLCNPGSGASYKEFLDKAENTGLKNMTIKVAIFITLTAPLYOSTQASQ 352

RESULT 8

US-08-838-151A-52
Sequence 52, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 353 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-52

Query Match 80.8%; Score 1566; DB 3; Length 353;
Best Local Similarity 80.1%; Pred. No. 7.6e-154;
Matches 282; Conservative 31; Mismatches 39; Indels 0; Gaps 0;

QY 1 MPPPKFRVQSKNYFLTYPCQSLSKERALSQLQNLTPVNNKFKIKICREIHENGEPHLAV 60
DB 1 MPPPKFRVQSKNYFLTYPCQSLSKERALSQLQNLTPVNNKFKIKICREIHENGEPHLAV 60
QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDYKSYIDKDGDTIEMGDFOIDG 120
DB 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDYKSYIDKDGDTIEMGDFOIDG 120
QY 121 RSARGGQOSANDSYAKALNAGVOSALAVAREOPKDFVLQNHINIRSNLERIFAKAPEPW 180
DB 121 RSARGGQOSANDSYAKALNAGVOSALAVAREOPKDFVLQNHINIRSNLERIFAKAPEPW 180
QY 181 VPPFOVSSFTNVDEMOMADNYFGTDAAPPRPVSIIVEGDSRTGKTWABALGPHNY 240
DB 181 VPPFOVSSFTNVDEMOMADNYFGTDAAPPRPVSIIVEGDSRTGKTWABALGPHNY 240
QY 241 LSGHLDPNHGVFNVDQVNYIDIAPIHYLKLKMKWELGAKQWQSNCKYKGPVQIKGI 300
DB 241 LSGHLDPNHGVFNVDQVNYIDIAPIHYLKLKMKWELGAKQWQSNCKYKGPVQIKGI 300
QY 301 PATVLCNPGSGASYKEFLDKAENTGLKNMTIKVAIFITLTAPLYOSTQASQ 352
DB 301 PATVLCNPGSGASYKEFLDKAENTGLKNMTIKVAIFITLTAPLYOSTQASQ 352

RESULT 9

US-08-838-151A-55
Sequence 55, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-616-5400
 TELEFAX: 312-616-5460
 INFORMATION FOR SEQ ID NO: 55:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 353 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-838-151A-55

Query Match 80.7%; Score 1564; DB 3; Length 353;
 Best Local Similarity 80.1%; Pred. No. 1,2e-153;
 Matches 282; Conservative 31; Mismatches 39; Indels 0; Gaps 0;

QY 1 MPPPKRRVQSKNYFLTYPCQSLSKERALSQLNLNTPVANKFKIKICRELHENGEPHLAV 60
 DB 1 MPPQRRVQSKNYFLTYPCPKPEVLSQLOKIHATNKKFKVCEERHENGEPHLA 60
 QY 61 LVPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKDGDTIEMGDFQIDG 120
 DB 61 LIQEGKFVCTNKRFLPLVSTRSAPHPNIOGAKSSDVKAYIDKGVITTEMGQFQVYG 120
 QY 121 RSARGQOQSANDSYAKALNAGVOSALAVLREOPKDFVLQNHINRSLERIFAKAPEPW 180
 DB 121 RSARGQOQSANDSYAKALNADSIRESALTILKEQPKDYVLQHNIRSLERIFKVEPEW 180
 QY 181 VPPFOVSSFTNVPEDEMADNYFGTDAAPDRPVSIIVEGDSRTGKTMMARALGPHN 240
 DB 181 VPPPLSSFTNVPMQEMWDDYFGRSAPARPERPISIIIEGDSRTGKTMMARALGPHN 240
 QY 241 LSGHLDNENGRVNSDVQYVVIDIAPHYLKLKHKMKELGAQDWQSNCKRYGKPVQIKG 300
 DB 241 LSGHLDNENGRVNSAVETNYIRDISPYLKLKHKMKELGAQDWQSNCKRYGKPVQIKG 300
 QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNTIKNAIFITLTAFLVQESTQASQ 352
 DB 301 PSIVLCNPGEGSSYKDFLDKEENRALHNTIHNAIFVTLTAFLVQSTQDCQ 352

RESULT 10
 US-08-809-103B-2
 Sequence 2, Application US/08809103B
 Patent No. 6133505
 GENERAL INFORMATION:
 APPLICANT: GROENBORN, Bruno
 TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: YOUNG & THOMPSON
 STREET: 745 South 23rd Street
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/809,103B
 FILING DATE: 17-MAR-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 94.11040
 FILING DATE: 15-SEP-1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: WO PCT/FR95/01192
 FILING DATE: 15-SEP-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: PATCH, Andrew J.
 REGISTRATION NUMBER: 32,925

REFERENCE/DOCKET NUMBER: US934AL CNR TOM
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (703) 521-2297
 TELEFAX: (703) 685-0573
 TELEX: 248425 EMBON
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 359 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-809-103B-2

Query Match 67.6%; Score 1311.5; DB 3; Length 359;
 Best Local Similarity 66.3%; Pred. No. 2.1e-127;
 Matches 240; Conservative 48; Mismatches 65; Indels 9; Gaps 4;

QY 1 MPPPKRRVQSKNYFLTYPCQSLSKERALSQLNLNTPVANKFKIKICRELHENGEPHLAV 60
 DB 1 MPPSGRISIAKRYFLTYPCDLTKENALSQLNTLQTPNKKFKIKICRELHENGEPHLA 60
 QY 61 LVPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKDGDTIEMGDFQIDG 120
 DB 61 LIQEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKGVITTEMGQFQIDG 120
 QY 121 RSARGQOQSANDSYAKALNAGVOSALAVLREOPKDFVLQNHINRSLERIFAKAPEPW 180
 DB 121 RSARGQOQIANDSYAKALNAGSKSQALDVYKELAPRDIYLFHNINSLDKVQVPAFY 180
 QY 181 VPPFOVSSFTNVPEDEMADNYFGTDAAPDRPVSIIVEGDSRTGKTMMARALGPHN 239
 DB 181 VSPFLSSFPQVDELEHWSENVMDA--AARWPRVSIIVEGDSRTGKTMMARALGPHN 238
 QY 240 YLSGHLDFNENGRVNSDVQYVVIDIAPHYLKLKHKMKELGAQDWQSNCKRYGKPVQIKG 299
 DB 239 YLSGHLDSQKVVSNNAVVIDVDVPHY--LKHFKEFMGAQDWQSNCKRYGKPVQIKG 296
 QY 300 IPAIVLCNPGEGASYKEFLDKAENTGLKNTIKNAIFITLTAFLVQESTQASQ 355
 DB 297 IPTFLCNPGQSSFKETLDEKQKQALKNATKNAIFVTHQPLFADTQNTTSHROEA 356
 QY 356 NQ 357
 DB 357 SE 358

RESULT 11
 US-08-809-103B-8
 Sequence 8, Application US/08809103B
 Patent No. 6133505
 GENERAL INFORMATION:
 APPLICANT: GROENBORN, Bruno
 TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
 TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
 NUMBER OF SEQUENCES: 17
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: YOUNG & THOMPSON
 STREET: 745 South 23rd Street
 CITY: Arlington
 STATE: Virginia
 COUNTRY: U.S.A.
 ZIP: 22202
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 OPERATING SYSTEM: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/809,103B
 FILING DATE: 17-MAR-1997
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: FR 94.11040

FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-8

Query Match 67.5%; Score 1308.5; DB 3; Length 359;
Best Local Similarity 66.0%; Pred. No. 4.2e-127;
Matches 239; Conservative 49; Mismatches 65; Indels 9; Gaps 4;

QY 1 MPPPKKFRVQSKNYFLTYPCSLSKSEALSQLONTLPVKKFKIKICRELHENGEPHLAV 60
DB 1 MPSSGRFSIAKKNYFLTYPCDLTKENALSQLONTLPVKKFKIKICRELHENGEPHLAI 60
QY 61 LVQFEGKYCTNNRFPDLVSPTRSAHFHPNIQAKSSSDVKSYYIDKDGDTIEGDFQIDG 120
DB 61 LIQFEGKYCTNNRFPDLVSPTRSAHFHPNIQAKSSSDVKSYYIDKDGDTIEGDFQIDG 120
QY 121 RSARGGQGSANDSYAKALNAGSVQALAVLREOPKDFVLQNHNRISNLERIFAKAPEPW 180
DB 121 RSARGGQGSANDSYAKALNAGSVQALAVLREOPKDFVLQNHNRISNLERIFAKAPEPW 180
QY 121 RSARGGQGSANDSYAKALNAGSVQALAVLREOPKDFVLQNHNRISNLERIFAKAPEPW 180
DB 121 RSARGGQGSANDSYAKALNAGSVQALAVLREOPKDFVLQNHNRISNLERIFAKAPEPW 180
QY 181 VPPFQVSSFTNVPMDEQEW-ADNYFGTGDAAPDRPVSIIVEGDSRTGKTMMARALGPHN 239
DB 181 VPPFQVSSFTNVPMDEQEW-ADNYFGTGDAAPDRPVSIIVEGDSRTGKTMMARALGPHN 239
QY 240 YLSGHLDFNGRVPSNDVQVNVIDDIAPHYLKLMKMKELGAQKQWQSNCKYKGPVQIKGG 299
DB 239 YLSGHLDFNGRVPSNDVQVNVIDDIAPHYLKLMKMKELGAQKQWQSNCKYKGPVQIKGG 299
QY 300 IPALVLCNPGEGASYPEFLDKAENTGLKNWTIKNAIFITLTAPLY-----QESTQASQETG 355
DB 297 IPTIFLCNPGQSSPFKEYLDEEKQALKNWATKNAIFVTIHQPLFADTNQNTTSHRQEEA 356
QY 356 NQ 357
DB 357 SE 358

RESULT 12
US-08-809-103B-4
Sequence 4, Application US/08809103B
Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GRONENBORN, Bruno
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-4

Query Match 67.3%; Score 1305.5; DB 3; Length 359;
Best Local Similarity 66.0%; Pred. No. 8.6e-127;
Matches 239; Conservative 48; Mismatches 66; Indels 9; Gaps 4;

QY 1 MPPPKKFRVQSKNYFLTYPCSLSKSEALSQLONTLPVKKFKIKICRELHENGEPHLAV 60
DB 1 MPSSGRFSIAKKNYFLTYPCDLTKENALSQLONTLPVKKFKIKICRELHENGEPHLAI 60
QY 61 LVQFEGKYCTNNRFPDLVSPTRSAHFHPNIQAKSSSDVKSYYIDKDGDTIEGDFQIDG 120
DB 61 LIQFEGKYCTNNRFPDLVSPTRSAHFHPNIQAKSSSDVKSYYIDKDGDTIEGDFQIDG 120
QY 121 RSARGGQGSANDSYAKALNAGSVQALAVLREOPKDFVLQNHNRISNLERIFAKAPEPW 180
DB 121 RSARGGQGSANDSYAKALNAGSVQALAVLREOPKDFVLQNHNRISNLERIFAKAPEPW 180
QY 121 RSARGGQGSANDSYAKALNAGSVQALAVLREOPKDFVLQNHNRISNLERIFAKAPEPW 180
DB 121 RSARGGQGSANDSYAKALNAGSVQALAVLREOPKDFVLQNHNRISNLERIFAKAPEPW 180
QY 181 VPPFQVSSFTNVPMDEQEW-ADNYFGTGDAAPDRPVSIIVEGDSRTGKTMMARALGPHN 239
DB 181 VPPFQVSSFTNVPMDEQEW-ADNYFGTGDAAPDRPVSIIVEGDSRTGKTMMARALGPHN 239
QY 240 YLSGHLDFNGRVPSNDVQVNVIDDIAPHYLKLMKMKELGAQKQWQSNCKYKGPVQIKGG 299
DB 239 YLSGHLDFNGRVPSNDVQVNVIDDIAPHYLKLMKMKELGAQKQWQSNCKYKGPVQIKGG 299
QY 300 IPALVLCNPGEGASYPEFLDKAENTGLKNWTIKNAIFITLTAPLY-----QESTQASQETG 355
DB 297 IPTIFLCNPGQSSPFKEYLDEEKQALKNWATKNAIFVTIHQPLFADTNQNTTSHRQEEA 356
QY 356 NQ 357
DB 357 SE 358

RESULT 13
US-08-809-103B-6
Sequence 6, Application US/08809103B
Patent No. 6133505
GENERAL INFORMATION:
APPLICANT: GRONENBORN, Bruno
TITLE OF INVENTION: PHYTOPATHOGENIC DNA VIRUS RESISTANT
TITLE OF INVENTION: TRANSGENIC PLANTS AND SEEDS AND METHODS FOR OBTAINING SAME
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: YOUNG & THOMPSON
STREET: 745 South 23rd Street
CITY: Arlington

STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,103B
FILING DATE: 17-MAR-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 94.11040
FILING DATE: 15-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/FR95/01192
FILING DATE: 15-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATCH, Andrew J.
REGISTRATION NUMBER: 32,925
REFERENCE/DOCKET NUMBER: USB94AL CNR TOM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 521-2297
TELEFAX: (703) 685-0573
TELEX: 248425 EMBON
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 359 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-809-103B-6

Query Match 67.3%; Score 1305.5; DB 3; Length 359;
Best Local Similarity 66.0%; Pred. No. 8.6e-127;
Matches 239; Conservative 48; Mismatches 66; Indels 9; Gaps 4;
QY 1 MPPEKFRVOSKNYFLTYPOCSLSKEBALSQLONTLPVKKFKIKICRELHENGEPHLHY 60
DB 1 MPRGRFSIKAKNYFLTYPKCDLTKENALSOITNLQTFPTNKLFIKICRELHENGEPHLHI 60
QY 61 LVQEGKYQCTNNRFFDLVSPTRSAHFHPNIQAKSSSDVKSITDKDGTIEMGDFOIDG 120
DB 61 LIQEGKYQCTNNRFFDLVSPTRSAHFHPNIQAKSSSDVKSITDKDGTIEMGDFOIDG 120
QY 121 RASAGGQOSANDSYAKALNAGSVOSALAVLREBPQDFVLONHNIRSNLERIFAKAPEPW 180
DB 121 RASAGGQOTANDAYAKALNAGSKQALDVIKELAPRDVLIHFHNINSNLDKVFVPPAPY 180
QY 181 VPPQVSSFTNVPEMOEM-ADNYFGTGDAPPRPVSIIVEGDSRTGKTWMAARALGPHN 239
DB 181 VSPFLSSFFDQVPEBLEHNSENVMDA--AAKPRPVSIVIEGDSRTGKTWMAARALGPHN 238
QY 240 YLSGHLDFNGRVSNDVOYVNIIDIAPIHYLKLKMKKELLGAQKQWQSNCKYKGPVQIKG 299
DB 239 YLQGLDLDSQKYVSNNAWYVNIIDVDPHY--LKHFKEPMGAQRDMQWSTKYGKPIQIKG 296
QY 300 IPAIVLCNPGEGASYKEFLDKAENTGKLNWITIKNAIFITLTAPLY---QESTQASQETG 355
DB 297 IPTFLCNPGQSSFFKEYLDEKQKQALKNMATKNAIFVTLIHQPLFADTNTTSHROBEA 356
QY 356 NQ 357
DB 357 SE 358

RESULT 14
US-08-838-151A-20
Sequence 20, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T

APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESS: Dressler, Rockey, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-20

Query Match 66.7%; Score 1293.5; DB 3; Length 357;
Best Local Similarity 66.3%; Pred. No. 1.5e-125;
Matches 238; Conservative 53; Mismatches 59; Indels 9; Gaps 4;
QY 4 PKFRVOSKNYFLTYPOCSLSKEBALSQLONTLPVKKFKIKICRELHENGEPHLHY 63
DB 2 PRLFKIYAKNYFLTYPCSLSKKEBALSQLKLEFPTNKYIKVCKELHENGEPHLHYLIQ 61
QY 64 PEGKYQCTNNRFFDLVSPTRSAHFHPNIQAKSSSDVKSITDKDGTIEMGDFOIDG 123
DB 62 PEGKYQCKNORFFDLVSPTRSAHFHPNIQAKSSTDKTYVEKDNFIDGVSQIDGRSA 121
QY 124 RGGQOSANDSYAKALNAGSVOSALAVLREBPQDFVLONHNIRSNLERIFAKAPEPW 183
DB 122 RGGQOSANDYAAALNAGSISEALNITKEKAPDYIIOFNLSNNDRIISPLEVYVSP 181
QY 184 FOVSSFTNVDEMOEM-ADNYFGTGDAPPRPVSIIVEGDSRTGKTWMAARALGPHN 242
DB 182 FLSSFFQVDEBLEHNSENV--VYSAARPMRPISIVIEGDSRTGKTWMAARALGPHN 239
QY 243 GHDPKGRVSNDOYVNIIDIAPIHYLKLKMKKELLGAQKQWQSNCKYKGPVQIKG 302
DB 240 GHLDLSPKYSNDNAWYVNIIDVDPHY--LKHFKEPMGAQRDMQWSTKYGKPIQIKG 297
QY 303 IVCNPGEGASYKEFLDKAENTGKLNWITIKNAIFITLTAPLY---QESTQASQETG 357
DB 298 IFLCNPGPTSSYREYLDKQKQALKNMATKNAIFVTLIEPLFASINQGPQDSQDET 356

RESULT 15
US-08-838-151A-24
Sequence 24, Application US/08838151A
Patent No. 6291743
GENERAL INFORMATION:
APPLICANT: Stout, John T

APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978
REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 357 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-24

Query Match 66.7%; Score 1293.5; DB 3; Length 357;
Best Local Similarity 66.3%; Pred. No. 1.5e-125;
Matches 238; Conservative 53; Mismatches 59; Indels 9; Gaps 4;

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DB 2 PRLFKIYAKNYFLTPVCSLSKEBALSQLKLEPTNKKYIKVCKELHNGEBPHLYLVQ 61
QY 64 FEKGYOCTNNRFPDIVSPTRSAHPHPIQAKSSSDVKSVIDKDGDTIEWGDFOIDGRSA 123
DB 62 FEKGYOCTNNRFPDLVSPNRSAPHPHPIQAKSSSDVKSVIDKDGDTIEWGDFOIDGRSA 121
QY 124 RGGQOSANDSYAKALNAGVOSALAVLREBPQDFVLONHINIRSNLERIPAKAPEPVPP 183
DB 122 RGGQOSANDYAKALNAGVOSALAVLREBPQDFVLONHINIRSNLERIPAKAPEPVPP 181
QY 184 FOVSSTFNVPDEMEW-ADNYFGTGAAPPDRPVSIIVEGDSRTGKTMARALGPHNYLS 242
DB 182 FLSSSFNQVDELEMEWAEV--VYSAPRPWRPISIVIEGDSRTGKTMARALGPHNYLC 239
QY 243 GHLDPFNGRVSNVOYVVIDDIAPHYLYKLKHWKELLGAOKWQSNCKYKGPVOIKGSI 302
DB 240 GHLDLPSPKYSNDAMVIVDDVDPHY--LKHFEFNGAQDWQSNCKYKGPVOIKGSIPT 297
QY 303 IYLCNPGEGASYKEFLDKAENTGKKNWTIKNAIFITLAPLY---QESTOASQETGNQ 357
DB 298 IYLCNPGEGASYKEFLDKAENTGKKNWTIKNAIFITLAPLY---QESTOASQETGNK 356

Search completed: December 3, 2004, 15:02:11
Job time: 24 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2004, 15:02:15 ; Search time 144 Seconds
(without alignments)
894.034 Million cell updates/sec

Title: US-09-491-063a-2

Sequence: 1 MEPPKFRVQSKNYFLTYPPQ.....PLYQSTQASQETGNQKAG 361

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1582122 seqs, 356623098 residues

Total number of hits satisfying chosen parameters: 1582122

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

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20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1902	98.1	361	US-08-838-151A-6	Sequence 6, Appl1
3	1892	97.6	361	US-08-838-151A-8	Sequence 8, Appl1
4	1886	97.3	361	US-08-838-151A-4	Sequence 4, Appl1
5	1572	81.1	353	US-08-838-151A-46	Sequence 46, Appl1
6	1572	81.1	353	US-08-838-151A-44	Sequence 44, Appl1
7	1567	80.8	353	US-08-838-151A-49	Sequence 49, Appl1
8	1566	80.8	353	US-08-838-151A-52	Sequence 52, Appl1
9	1564	80.7	353	US-08-838-151A-55	Sequence 55, Appl1
10	1504.5	77.6	352	US-10-633-850-80	Sequence 80, Appl1
11	1503.5	77.5	352	US-10-633-850-84	Sequence 84, Appl1
12	1502.5	77.5	352	US-10-633-850-1	Sequence 1, Appl1
13	1502.5	77.5	352	US-10-633-850-64	Sequence 64, Appl1

14	1500.5	77.4	352	US-10-633-850-86	Sequence 86, Appl1
15	1499.5	77.3	352	US-10-633-850-82	Sequence 82, Appl1
16	1499.5	77.3	352	US-10-633-850-92	Sequence 92, Appl1
17	1499.5	77.3	352	US-10-633-850-94	Sequence 94, Appl1
18	1499	77.3	356	US-09-289-346A-11	Sequence 11, Appl1
19	1497.5	77.2	352	US-10-633-850-90	Sequence 90, Appl1
20	1496.5	77.2	352	US-10-633-850-58	Sequence 58, Appl1
21	1496.5	77.2	352	US-10-633-850-88	Sequence 88, Appl1
22	1496.5	77.2	352	US-10-633-850-98	Sequence 98, Appl1
23	1495.5	77.1	352	US-10-633-850-76	Sequence 76, Appl1
24	1494.5	77.1	352	US-10-633-850-68	Sequence 68, Appl1
25	1494.5	77.1	352	US-10-633-850-96	Sequence 96, Appl1
26	1492.5	77.0	352	US-10-633-850-62	Sequence 62, Appl1
27	1492.5	77.0	352	US-10-633-850-78	Sequence 78, Appl1
28	1490.5	76.9	352	US-10-633-850-74	Sequence 74, Appl1
29	1488.5	76.8	352	US-10-633-850-52	Sequence 52, Appl1
30	1488.5	76.8	352	US-10-633-850-66	Sequence 66, Appl1
31	1487.5	76.7	352	US-10-633-850-56	Sequence 56, Appl1
32	1486.5	76.7	352	US-10-633-850-60	Sequence 60, Appl1
33	1485.5	76.6	352	US-10-633-850-72	Sequence 72, Appl1
34	1480.5	76.4	352	US-10-633-850-54	Sequence 54, Appl1
35	1478.5	76.3	352	US-10-633-850-70	Sequence 70, Appl1
36	1293.5	66.7	357	US-08-838-151A-20	Sequence 20, Appl1
37	1293.5	66.7	357	US-08-838-151A-24	Sequence 24, Appl1
38	1290.5	66.6	357	US-08-838-151A-30	Sequence 30, Appl1
39	1288.5	66.5	357	US-08-838-151A-107	Sequence 107, Appl1
40	1230.5	63.5	349	US-10-633-850-112	Sequence 112, Appl1
41	1225.5	63.2	349	US-10-633-850-112	Sequence 112, Appl1
42	661	34.1	131	US-08-838-151A-14	Sequence 14, Appl1
43	486	25.1	335	US-10-151-336-6	Sequence 3, Appl1
44	275.5	14.2	293	US-10-151-336-3	Sequence 602, Appl1
45	257	13.3	264	US-10-310-154-602	

ALIGNMENTS

RESULT 1
US-08-838-151A-2
; Sequence 2, Application US/08838151A
; Publication No. US20010011379A1
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Liu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing Geminitiviruses
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dressler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-2

Query Match 98.4%; Score 1908; DB 8; Length 361;
Best Local Similarity 98.3%; Pred. No. 1,1e-162;
Matches 355; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

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DB 1 MPPKFFRVOSKNYFLTYPCSSLSKEBALSQLONTLPVKKFKIKICREHENGEPHLAV 60
QY 61 LVQFEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSSDVKSVIDKDGDTIEWGDFQIDG 120
DB 61 LVQFEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSSDVKSVIDKDGDTIEWGDFQIDG 120
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DB 121 RSARGGQGSANDSYAKALNAGSVOSALAVLREOPKDFVLQNNHRSNLERIFAKAPEPW 180
QY 181 VPPFOVSSFTNVDEMOMADNYFGTGDAAPDRPVSIIVEGSRGTGTMARALGPHNY 240
DB 181 VPPFOVSSFTNVDEMOMADNYFGTGDAAPDRPVSIIVEGSRGTGTMARALGPHNY 240
QY 241 LSGHLDNFRVFSNDVQYNYIDIAPIHYLKLKMKKELLGAQXQWQSNCKYKGPVQIKGI 300
DB 241 LSGHLDNFRVFSNDVQYNYIDIAPIHYLKLKMKKELLGAQXQWQSNCKYKGPVQIKGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQSTQASQETGNQKQ 360
DB 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQSTQASQETGNQKQ 360
QY 361 G 361
DB 361 G 361

RESULT 2
US-08-838-151A-6
Sequence 6, Application US/08838151A
Publication No. US20010011379A1
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSES: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Mueller, Lisa V
REGISTRATION NUMBER: 38,978

REFERENCE/DOCKET NUMBER: SVS3801P0260
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
TELEFAX: 312-616-5460
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 361 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-838-151A-6

Query Match 98.1%; Score 1902; DB 8; Length 361;
Best Local Similarity 98.1%; Pred. No. 3,8e-162;
Matches 354; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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DB 1 MPPKFFRVOSKNYFLTYPCSSLSKEBALSQLONTLPVKKFKIKICREHENGEPHLAV 60
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DB 61 LVQFEGKYQCTNNRFPDLVSPTRSAHPHPIQAKSSSDVKSVIDKDGDTIEWGDFQIDG 120
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DB 121 RSARGGQGSANDSYAKALNAGSVOSALAVLREOPKDFVLQNNHRSNLERIFAKAPEPW 180
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DB 181 VPPFOVSSFTNVDEMOMADNYFGTGDAAPDRPVSIIVEGSRGTGTMARALGPHNY 240
QY 241 LSGHLDNFRVFSNDVQYNYIDIAPIHYLKLKMKKELLGAQXQWQSNCKYKGPVQIKGI 300
DB 241 LSGHLDNFRVFSNDVQYNYIDIAPIHYLKLKMKKELLGAQXQWQSNCKYKGPVQIKGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQSTQASQETGNQKQ 360
DB 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQSTQASQETGNQKQ 360
QY 361 G 361
DB 361 G 361

RESULT 3
US-08-838-151A-8
Sequence 8, Application US/08838151A
Publication No. US20010011379A1
GENERAL INFORMATION:
APPLICANT: Stout, John T
APPLICANT: Luu, Hang T
APPLICANT: Maxwell, Douglas
APPLICANT: Ahlquist, Paul
APPLICANT: Hanson, Steve
TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
TITLE OF INVENTION: Genes
NUMBER OF SEQUENCES: 63
CORRESPONDENCE ADDRESSES:
ADDRESSES: Dressler, Rocky, Milnamow & Katz
STREET: Two Prudential Plaza, Suite 4700
CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,151A
FILING DATE:

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/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mueller, Lisa V
/ REGISTRATION NUMBER: 38,978
/ REFERENCE/DOCKET NUMBER: SVS801P0260
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-616-5400
/ TELEFAX: 312-616-5460
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 361 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULAR TYPE: protein
/ US-08-838-151A-8

Query Match      97.6%; Score 1892; DB 8; Length 361;
Best Local Similarity 97.8%; Pred. No. 3e-161;
Matches 353; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

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DB 361 G 361

RESULT 4
US-08-838-151A-4
/ Sequence 4, Application US/08838151A
/ Publication No. US20010011379A1
/ GENERAL INFORMATION:
/ APPLICANT: Stout, John T
/ APPLICANT: Lau, Hang T
/ APPLICANT: Maxwell, Douglas
/ APPLICANT: Ahlquist, Paul
/ APPLICANT: Hanson, Steve
/ TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
/ NUMBER OF SEQUENCES: 63
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dressler, Rocky, Milanow & Katz
/ STREET: Two Prudential Plaza, Suite 4700
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: U.S.A.
/ ZIP: 60601
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
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/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/838,151A
/ FILING DATE:
/ CLASSIFICATION: 800
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Mueller, Lisa V
/ REGISTRATION NUMBER: 38,978
/ REFERENCE/DOCKET NUMBER: SVS3801P0260
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 312-616-5400
/ TELEFAX: 312-616-5460
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 361 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULAR TYPE: protein
/ US-08-838-151A-4

Query Match      97.3%; Score 1886; DB 8; Length 361;
Best Local Similarity 97.5%; Pred. No. 1e-160;
Matches 352; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 1 MPPPKFRVQSKNYFLTYPCSLSKKEALSQLONLTPVKKFKIKCRELHENGEPHLHY 60
DB 1 MPPPKFRVQSKNYFLTYPCSLSKKEALSQLONLTPVKKFKIKCRELHENGEPHLHY 60
QY 61 LVQFEKRYCTNNRFPDLVSPTRSAHFHPIQAKSSDVKSITIDGDTIEWGDFQIDG 120
DB 61 LVQFEKRYCTNNRFPDLVSPTRSAHFHPIQAKSSDVKSITIDGDTIEWGDFQIDG 120
QY 121 RSARGGQGSANDSYAKALNAGSVQSLAVLREOPKDFVLQNNHINSNLERIPAKAPBPW 180
DB 121 RSARGGQGSANDSYAKALNAGSVQSLAVLREOPKDFVLQNNHINSNLERIPAKAPBPW 180
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DB 181 VPPFQVSSFTNVDEQEWADNYFGTGAAPRPPVSIIVEGDSRTGKTMMARALGPBNY 240
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DB 241 LSGHLDPNRVRVNDVQYVINDIAPHYLKLMKMKELGAQKDMQSNCKYKGVQIKGGI 300
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DB 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQSTQASQETGNQKQ 360
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DB 361 G 361

RESULT 5
US-08-838-151A-44
/ Sequence 44, Application US/08838151A
/ Publication No. US20010011379A1
/ GENERAL INFORMATION:
/ APPLICANT: Stout, John T
/ APPLICANT: Lau, Hang T
/ APPLICANT: Maxwell, Douglas
/ APPLICANT: Ahlquist, Paul
/ APPLICANT: Hanson, Steve
/ TITLE OF INVENTION: Transgenic Plants Expressing Geminiivirus
/ NUMBER OF SEQUENCES: 63
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Dressler, Rocky, Milanow & Katz
/ STREET: Two Prudential Plaza, Suite 4700
/ CITY: Chicago
/ STATE: Illinois
/ COUNTRY: U.S.A.
/ ZIP: 60601
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; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-44

```

```

Query Match      81.1%; Score 1572; DB 8; Length 353;
Best Local Similarity 80.4%; Pred. No. 1,7e-132;
Matches 283; Conservative 31; Mismatches 38; Indels 0; Gaps 0;

```

```

QY 1 MPPPKFRVQSKNYFLTYPOCSLSKEBALSQLQNLNTPVKKIKICREHENGEPHLAV 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 MPPPKFRVQSKNYFLTYPRCPPIKEBVLSQLQKHATATKKIKVCEERHENGEPHLA 60
QY 61 LVQFEGVQCTNNRFPDLVPTSAHFHPNIQAKSSDVKSYIDKQDGTIENGDFQIDG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 LIQFEGFVCTNNRFLDLVSTSAHPHPNIQAKSSDVKAYIDKQVITIEGQFQVDG 120
QY 121 RSARGGQGSANDSYAKALNAGVOSALAVIREQPKDFVLQNNHNSLNERIPAKAEPW 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 RSARGGQGSANDSYAKALNADSIESTALTILKEQPKDYVLQNNHNSLNERIPAKAEPW 180
QY 181 VPPQVSSFTNVDPDEQEMADNTFGTGDAAAPRRPVSIIVEGDSRTGKTMAALGPHNY 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 181 VPPPLSSFTNVDPDEQEMADNTFGTGDAAAPRRPVSIIVEGDSRTGKTMAALGPHNY 240
QY 241 LSGHLDPNGVFVNDVQYNYIDIDAPHYLKLKMKKELIGAQKQMSCKTGKPVQIKGI 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 241 LSGHLDPNRSVYNAVAEYNYIDIDISPNYLLKMKKELIGAQKQMSCKTGKPVQIKGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTQASQ 352
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 301 PSIVLCNPGEGSSYKDFLDKENRALHNTIHNALFVTLTAPLYQSTTQDCQ 352

```

```

RESULT 6
US-08-838-151A-46
; Sequence 46, Application US/08838151A
; Publication No. US20010011379A1
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlgquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing GeminiViruses
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dresler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 46:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-46

```

```

Query Match      81.1%; Score 1572; DB 8; Length 353;
Best Local Similarity 80.4%; Pred. No. 1,7e-132;
Matches 283; Conservative 31; Mismatches 38; Indels 0; Gaps 0;

```

```

QY 1 MPPPKFRVQSKNYFLTYPOCSLSKEBALSQLQNLNTPVKKIKICREHENGEPHLAV 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 MPPPKFRVQSKNYFLTYPRCPPIKEBVLSQLQKHATATKKIKVCEERHENGEPHLA 60
QY 61 LVQFEGVQCTNNRFPDLVPTSAHFHPNIQAKSSDVKSYIDKQDGTIENGDFQIDG 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 LIQFEGFVCTNNRFLDLVSTSAHPHPNIQAKSSDVKAYIDKQVITIEGQFQVDG 120
QY 121 RSARGGQGSANDSYAKALNAGVOSALAVIREQPKDFVLQNNHNSLNERIPAKAEPW 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 RSARGGQGSANDSYAKALNADSIESTALTILKEQPKDYVLQNNHNSLNERIPAKAEPW 180
QY 181 VPPQVSSFTNVDPDEQEMADNTFGTGDAAAPRRPVSIIVEGDSRTGKTMAALGPHNY 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 181 VPPPLSSFTNVDPDEQEMADNTFGTGDAAAPRRPVSIIVEGDSRTGKTMAALGPHNY 240
QY 241 LSGHLDPNGVFVNDVQYNYIDIDAPHYLKLKMKKELIGAQKQMSCKTGKPVQIKGI 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 241 LSGHLDPNRSVYNAVAEYNYIDIDISPNYLLKMKKELIGAQKQMSCKTGKPVQIKGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTQASQ 352
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 301 PSIVLCNPGEGSSYKDFLDKENRALHNTIHNALFVTLTAPLYQSTTQDCQ 352

```

```

RESULT 7
US-08-838-151A-49
; Sequence 49, Application US/08838151A
; Publication No. US20010011379A1
; GENERAL INFORMATION:
; APPLICANT: Stout, John T
; APPLICANT: Luu, Hang T
; APPLICANT: Maxwell, Douglas
; APPLICANT: Ahlgquist, Paul
; APPLICANT: Hanson, Steve
; TITLE OF INVENTION: Transgenic Plants Expressing GeminiViruses
; TITLE OF INVENTION: Genes
; NUMBER OF SEQUENCES: 63
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dresler, Rocky, Milnamow & Katz
; STREET: Two Prudential Plaza, Suite 4700
; CITY: Chicago
; STATE: Illinois
; COUNTRY: U.S.A.
; ZIP: 60601

```

```

? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: PatentIn Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/838,151A
? FILING DATE:
? CLASSIFICATION: 800
? ATTORNEY/AGENT INFORMATION:
? NAME: Mueller, Lisa V
? REGISTRATION NUMBER: 38,978
? REFERENCE/DOCKET NUMBER: SWS3801P0260
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-616-5400
? TELEFAX: 312-616-5460
? INFORMATION FOR SEQ ID NO: 49:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 353 amino acids
? TYPE: amino acid
? TOPOLOGY: linear
? MOLECULE TYPE: protein
? OS-08-838-151A-49

```

Query Match	80.8%	Score 1567	DB 8	Length 353
Best Local Similarity	80.1%	Pred No. 4.8e-132		
Matches 282	Conservative 31	Mismatches 39	Indels 0	Gaps 0

Qy	1	MPKKKKRVSQKNVFLTYQCSLSKEEALSCQJONTNTPVNNKKFLIKICELHENEPHIV	60
Db	1	MPPKQFRVQSNNVFLTYRCPRIKKEEVLSTQJQKHTNTNKKFLIKVCEERHENEPHIHA	60
Qy	61	LVOPEKTCQCTNNRFPDVLVSPTRSAHFHNPICGASSSDVKSXYIDKDGDTLEMGDFQIDG	120
Db	61	LIQEKPFCVCTNNRFLDVLVSSTRSAFPHNPICGASSSDVAYAYIDKGVITLBMQFQVDDG	120
Qy	121	RSARGGQOSANDSYAVALNAGSVQSAALATRECEPKDVLVLONNHNRSLERIRPAKAEPEW	180
Db	121	RSARGGQOSANDSYAVALNADSIESALTILKEGQKDYVLQHHNIRSLERIRFKVYPEPW	180
Qy	181	VPPFOVSSFINNPDEMEQWADNIFCTGDAAPRDPVSVITVEGDSFTGKTMARALGPHNY	240
Db	181	VPPFPLSSFINNPVNMQEWDDYFEGGSAARPERISITIVGDSKTGKTMARALGPHNY	240
Qy	241	LSGHLDFNGSVFSNDQVNVYIDDIAPHYKLKGWELLGAQKDWQSNCKYGPQVIRGGI	300
Db	241	LSGHLDFNGSVSNAYEVYIDDISPNYKLKGWELLGAQKDWQSNCKYGPQVIRGGI	300
Qy	301	PAIVLCNPGEGASVKEFLDKAENTGLKNTTIGNALFITLTPAPVQESVQASQ	352
Db	301	PSIVLCNPGEGASSVQDFDKESNRALHNTTIGNALFVTLTPAPVQESTYDQDQ	352

US-RESULT 8 151A-52
: Sequence 52, Application US/08838151A
: Publication No. US20010011379A1
: GENERAL INFORMATION:
: APPLICANT: Scout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: APPLICANT: Hanson, Steve
: TITLE OF INVENTION: Transgenic Plants Expressing GeminiVirus
: TITLE OF INVENTION: Genes
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601

```

1  COMPUTER READABLE FORM:
2  MEDIUM TYPE: Floppy disk
3  COMPUTER: IBM PC compatible
4  OPERATING SYSTEM: PC-DOS/MS-DOS
5  SOFTWARE: PatentIn Release #1.0, Version #1.30
6  CURRENT APPLICATION DATA:
7  APPLICATION NUMBER: US/09/839,151A
8  FILING DATE:
9  CLASSIFICATION: 800
10 ATTORNEY/AGENT INFORMATION:
11 NAME: Mueller, Lisa V
12 REGISTRATION NUMBER: 38,978
13 REFERENCE/DOCKET NUMBER: SYS3801P0260
14 TELECOMMUNICATION INFORMATION:
15 TELEPHONE: 312-616-5400
16 TELEFAX: 312-616-5460
17 INFORMATION FOR SEQ ID NO: 52:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH: 353 amino acids
20 TYPE: amino acid
21 TOPOLOGY: linear
22 MOLECULE TYPE: protein
23 US-08-839-151A-52

```

Query Match	80.8%	Score 1566;	DB 8;	Length 353;
Best Local Similarity	80.1%	Pred. No. 5	8e-132;	
Matches 282;	Conservative 31;	Mismatches 39;	Indels 0;	Gaps 0

Qy	1	MPPEKPFVSGKNELTYPOCSLSKEEALSLOLONTPNKKFKICRLAHNGEHEHLY	60
Dp	1	MPPEQRFVSGKNFLTYPRCPRIPEBEVLSQLOQHTHTANKKFKIYVCSEBHEHGEPHHLYA	60
Qy	61	LVQREBKQCTNNRPFDDVSTPSRAHAFHPNIQGAASSSDVASYIDKGGTITWEDPQIDG	120
Dp	61	LIQEGKRCVCKNKLFDLVSSSTRSAFPHHPNIQGAASSSDVAKYIDKDGVTIEWGQOVLGQ	120
Qy	121	RSARGGQOASNDASYAKALNAGSVOSALALVREBPCKDPEVLQNHNRISMLERIFAKAPBPM	180
Dp	121	RSARGGQOASNDASYAKALNADSISSALFTILKEBQKDYVLQHNHRSNLERIFAKPEBPM	180
Qy	181	VPPPVQSSFTNVPEBMOQMANNYTGTGAAAPDRVSVIIVGEDSTRTGKTMARALGPHNY	240
Dp	181	VPPPLSSFINVPMQEMWDVDTGGRGSAAPERPISIIIVEDSDTGHTMMARALGPHNY	240
Qy	241	LSGLHDFNGRVSFNDVQYVNIIDILAPHLKTKHWEELIGAQOMQOSNCKYGRPVQIKGSI	300
Dp	241	LSGLHDFNRSRYNAVEYVNIIDISPNYVLKJHWEELIGAQOMQOSNCKYGRPVQIKGSI	300
Qy	301	PATVLCNPGEGASRYKEPLDKAKENGLKMWTKIKNAFITLTLAPLYQESTQASQ	352
Dp	301	PSIYLCNPGEGESSYKDFLDKEENRLAHMTTINHALFVTLTAPLYQESTTQDCQ	352

RESULT 9
US-08-838-151A-55
: Sequence 55, Application US/08838151A
: Publication No. US20010011379A1
: GENERAL INFORMATION:
: APPLICANT: Scout, John T
: APPLICANT: Luu, Hang T
: APPLICANT: Maxwell, Douglas
: APPLICANT: Ahlquist, Paul
: TITLE OF INVENTION: Transgenic Plants Expressing Geminivirus
: TITLE OF INVENTION: Genes
: NUMBER OF SEQUENCES: 63
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Dressler, Rocky, Milnamow & Katz
: STREET: Two Prudential Plaza, Suite 4700
: CITY: Chicago
: STATE: Illinois
: COUNTRY: U.S.A.
: ZIP: 60601

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838,151A
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Mueller, Lisa V
; REGISTRATION NUMBER: 38,978
; REFERENCE/DOCKET NUMBER: SVS3801P0260
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-616-5400
; TELEFAX: 312-616-5460
; INFORMATION FOR SEQ ID NO: 55:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 353 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-838-151A-55

```

```

Query Match      80.7%; Score 1564; DB 8; Length 353;
Best Local Similarity 80.1%; Pred. No. 8.8e-132;
Matches 287; Conservative 31; Mismatches 39; Indels 0; Gaps 0;

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```

QY 1 MPPPKFRVQSKNYFLTYPCSLSKKEALSQALNTLPVKKFKIKICREIHNGEPHLAV 60
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 MPPPKFRVQSKNYFLTYPCSLSKKEALSQALNTLPVKKFKIKICREIHNGEPHLA 60
QY 61 LVQPEGKYQCTNNRFFDLVSPTRSAHFHPNIOGAKSSDVKSYIDKGDPTIEMGDFOID 120
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 61 LVQPEGKYQCTNNRFFDLVSPTRSAHFHPNIOGAKSSDVKAYIDKGDPTIEMGDFOID 120
QY 121 RSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEPW 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 RSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEPW 180
QY 121 RSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEPW 180
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 121 RSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEPW 180
QY 181 VPPFQVSSFTNVPEDEMGADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 181 VPPFQVSSFTNVPEDEMGADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
QY 181 VPPFQVSSFTNVPEDEMGADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 181 VPPFQVSSFTNVPEDEMGADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
QY 241 LSGHLDENGRVFSNDVQYVVIDIAPHYLLKHKMKELIGAQRQWQSNCKYKGPVQIKGGI 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 241 LSGHLDENGRVFSNDVQYVVIDIAPHYLLKHKMKELIGAQRQWQSNCKYKGPVQIKGGI 300
QY 241 LSGHLDENGRVFSNDVQYVVIDIAPHYLLKHKMKELIGAQRQWQSNCKYKGPVQIKGGI 300
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 241 LSGHLDENGRVFSNDVQYVVIDIAPHYLLKHKMKELIGAQRQWQSNCKYKGPVQIKGGI 300
QY 301 PAIVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTOASQ 352
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 301 PAIVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTOASQ 352
QY 301 PAIVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTOASQ 352
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 301 PAIVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTOASQ 352

```

```

RESULT 10
US-10-633-850-80
; Sequence 80, Application US/10633850
; Publication No. US20040205843A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Grubisem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633, 850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 80
; LENGTH: 352

```

```

; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; US-10-633-850-80

```

```

Query Match      77.6%; Score 1504.5; DB 17; Length 352;
Best Local Similarity 75.9%; Pred. No. 2e-126;
Matches 267; Conservative 44; Mismatches 40; Indels 1; Gaps 1;

```

```

QY 1 MPPPKFRVQSKNYFLTYPCSLSKKEALSQALNTLPVKKFKIKICREIHNGEPHLH 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 MPPPKFRVQSKNYFLTYPCSLSKKEALSQALNTLPVKKFKIKICREIHNGEPHLH 60
QY 60 LVQPEGKYQCTNNRFFDLVSPTRSAHFHPNIOGAKSSDVKSYIDKGDPTIEMGDFOID 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 60 LVQPEGKYQCTNNRFFDLVSPTRSAHFHPNIOGAKSSDVKSYIDKGDPTIEMGDFOID 120
QY 120 GRSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEP 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 120 GRSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEP 180
QY 180 VPPFQVSSFTNVPEDEMGADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTMMARALGPHN 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 180 VPPFQVSSFTNVPEDEMGADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTMMARALGPHN 240
QY 240 YLSGHLDENGRVFSNDVQYVVIDIAPHYLLKHKMKELIGAQRQWQSNCKYKGPVQIKGG 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 240 YLSGHLDENGRVFSNDVQYVVIDIAPHYLLKHKMKELIGAQRQWQSNCKYKGPVQIKGG 240
QY 300 IPAILVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTOAS 351
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 300 IPAILVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTOAS 352
QY 301 PAIVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTOAS 352
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 301 PAIVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTOAS 352

```

```

RESULT 11
US-10-633-850-84
; Sequence 84, Application US/10633850
; Publication No. US20040205843A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Grubisem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 84
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
; US-10-633-850-84

```

```

Query Match      77.5%; Score 1503.5; DB 17; Length 352;
Best Local Similarity 75.9%; Pred. No. 2.4e-126;
Matches 267; Conservative 45; Mismatches 39; Indels 1; Gaps 1;

```

```

QY 1 MPPPKFRVQSKNYFLTYPCSLSKKEALSQALNTLPVKKFKIKICREIHNGEPHLH 59
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 1 MPPPKFRVQSKNYFLTYPCSLSKKEALSQALNTLPVKKFKIKICREIHNGEPHLH 60
QY 60 LVQPEGKYQCTNNRFFDLVSPTRSAHFHPNIOGAKSSDVKSYIDKGDPTIEMGDFOID 119
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 60 LVQPEGKYQCTNNRFFDLVSPTRSAHFHPNIOGAKSSDVKSYIDKGDPTIEMGDFOID 120
QY 120 GRSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEP 179
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 120 GRSARGGQGSANDSYAKALNAGVQSALAVLREOPKDFVLQNHNRISNLERIPAKAPEP 180
QY 180 VPPFQVSSFTNVPEDEMGADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTMMARALGPHN 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 180 VPPFQVSSFTNVPEDEMGADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTMMARALGPHN 240
QY 240 YLSGHLDENGRVFSNDVQYVVIDIAPHYLLKHKMKELIGAQRQWQSNCKYKGPVQIKGG 239
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 240 YLSGHLDENGRVFSNDVQYVVIDIAPHYLLKHKMKELIGAQRQWQSNCKYKGPVQIKGG 240
QY 300 IPAILVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTOAS 351
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 300 IPAILVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTOAS 352
QY 301 PAIVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTOAS 352
   |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
DB 301 PAIVLCNPEGASYSKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTOAS 352

```



```

OY      180  WPPPVQVSSFTNVPEMEMOAMNRYGCTGAAPDPDRVSTIIVEGDSGTGTMARALGPHN 239
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      181  WLPPEHVSFTNVPEEMKOMAENYFGKSSAAPPERISIIIEBDSGTGTMARSLGPHN 240
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      240  YLSGHLDFNGRVFSNDVOYVNIIDIAPHYLKJLKHWEKLLGAOKDWQSNCKRYKPVQIKG 239
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      241  YLSGHLDFNSRYVSNKVEYVNIIDVTPQYLKLKHWEKELIGAQRDWQTNCKRYKPVQIKG 300
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
OY      300  IPAIVLCNPGEGASGYKEFLDKAKENTGKRWITKNAIFITLTAPLYBESTQAS 351
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      301  IPSIVLCNPGEGASYKVFLDKEENTPLKRWITPNAKVFLNSPLYOSTQSS 352
      |||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 12
US-10-633-850-1
Sequence 1, Application US/10633850
Publication No. US20040205843A1
GENERAL INFORMATION:
APPLICANT: Hanley-Bowdoin, Linda
APPLICANT: Orozco, Beverly M.
APPLICANT: Grisseem, Wilhelm
TITLE OR INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
FILE REFERENCE: 5051.4581P
CURRENT APPLICATION NUMBER: US/10/633, 850
CURRENT FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 09/289, 346
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 60/125,004
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 352
TYPE: PRT
ORGANISM: Tomato golden mosaic virus
US-10-633-850-1

```

Query Match	77.5%;	Score 1502.5;	DB 17;	Length 352;
Best Local Similarity	75.9%;	Pred. No. 3e-126;		
Matches 267;	Conservative 44;	Mismatches 40;	Indels 1;	Gaps 1

Qy	1	MP- -PKRRVYQKVEFLTPYPCSSLSKEEALSQLONTNTVNNKFKIKICELHENGEPHL 59
		: : : : : : : : : : : : : : : : : : : : : : : : :
Db	1	MPSHKRFQINAKNVEFLTPYPCSSLSKEEALSQLOANTNTINKFKIKICELHEDGGPHL 60
		: : : : : : : : : : : : : : : : : : : : : : : : :
Qy	60	VLVQEGKGYCCNNNPFDDLVPSTRSAHFHPNIGAKSSSDVKSVIDKDGTTIEWGQFOID 119
		: : : : : : : : : : : : : : : : : : : : : : : : :
Db	61	VLIQEGKGYCCNNQPFDDLVPSTRSAHFHPNIGORASSSDVKYIIDKGGTLWGEFOVD 120
		: : : : : : : : : : : : : : : : : : : : : : : : :
Qy	120	GRSARGGQGSANDSYAKALNAGSVOSALATVLRKECPKDFVLQNHNIRSNLIERIFARAPB 179
		: : : : : : : : : : : : : : : : : : : : : : : : :
Db	121	GRSARGGGQTSNDLAAAEALNAGSKKEALOITREKIDPEKTLPOCHNLNSNIDRIFDPTPER 180
		: : : : : : : : : : : : : : : : : : : : : : : : :
Qy	180	WVPPEQVSSFNTVPDEMOEWADNYFGTGDAAFPDRPVSIIIVEGDSRTGKTMARALGPHN 239
		: : : : : : : : : : : : : : : : : : : : : : : : :
Db	181	WLPPEHVSFTNVPEDMQMAENYFGKSAAPRERISIIIEGDSRTGKTMARSLGPHN 240
		: : : : : : : : : : : : : : : : : : : : : : : : :
Qy	240	YLSGHLDPNGRYFESNDVQRYNVIDIAPHYLKLNKMKELLGAQCDWQSNCKYKGPVOIKG 299
		: : : : : : : : : : : : : : : : : : : : : : : : :
Db	241	YLSGHLDLNSRYSYKKEYNVVIDVTPQYLKLNKMKELLGAQCDWQNTCKYKGPVOIKG 300
		: : : : : : : : : : : : : : : : : : : : : : : : :
Qy	300	IPATVLCNPGEGASYKEFLDKAENLGKKNWTIKNAIFITLTPAVLYOESTQAS 351
		: : : : : : : : : : : : : : : : : : : : : : : : :
Db	301	IPSTVLCNPGEGASYKVELDKENETPLKWNTHNAFVELNSLYOESTQSS 352
		: : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
US-10-633-850-64
; Sequence 64, Application US/10633850
; Publication No. US20040205843A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.

```

APPLICANT: Grunseem, Miltheim
TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
FILE REFERENCE: 5051.4581P
CURRENT APPLICATION NUMBER: US/10/633,850
PRIORITY FILING DATE: 2003-08-04
PRIOR APPLICATION NUMBER: US 09/289,346
PRIOR FILING DATE: 1999-04-09
PRIOR APPLICATION NUMBER: US 60/125,004
PRIOR FILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 112
SOFTWARE: PatentIn version 3.2
SEQ ID NO 64
/
/
LENGTH: 352
/
/
TYPE: PR1
/
/
ORGANISM: Tomato golden mosaic virus
US-10-633-850-64

```

Query Match	77.5%;	Score 1502.5;	DB 17;	Length 352;
Best Local Similarity	75.9%;	Pred. No. 3e-126;		
Matches 267; Conservative	44;	Mismatches 40;	Indels 1;	Gaps 1;

Qy	1	MP-PKFERVOSKNVFLTYEQCSJSKREALSOLONTLPVKKRITKICREIHEHGEPLH	59
Db	1	MPSHKGFQJNANKVFLTYEQCSJSKREBSLQJALNTPINKKRIKICREIHEHGGPHH	60
Qy	60	VLVQPEKRYOCTNNREFDLVSPTRSAFHFNIGCAKSSPVKSYIDMDGPTIEMGDIOID	119
Db	61	VLIQPEKRYCCONRFPDLVSPTRSAPFHFNIOAKSSSDVKTYIIDXGDTLWGEBOVD	120
Qy	120	GRSARGQOSANDSYAFALNAGSVOSALAVIREOPDFVLONHNIRSNLERIPAKAPEP	179
Db	121	GRSARGGQJNSDPAALNALNASSAAALQIIRKIKPEKTYQFQHNLSMNDRIPIDKTPEP	180
Qy	180	WVPEFOVSSFPNNVEDMOWEADNYFCFGDGAAPRPSVITVEGDSRGTMMARALCPHN	239
Db	181	WLPFPFHSSFFPNVDEMRQMAENFGGSSAARPERPSIIEGDSRGTMMASLSLCPHN	240
Qy	240	YLSGHLDFNGRVFSNDQYVNVYIDIAHYLYLTKMKKELLGAOKDMQSNCKRYGKVPQIKG	299
Db	241	YLSGHLDLNSKVSXNKYEVNVYIDVTPQYKTLKMKKELIGAORDMOTNCKRYGKVPQIKG	300
Qy	300	IPAVILNPNBPGASYKEFLDKAENTGKMMTIKARIPITLTAPLYOSTOSAS	351
Db	301	IPSVILNPNBPGASYKVLKREKENTPILKMMTFHNAKVFANSPLYOSTOSAS	352

```

RESULT 14
US-10-633-850-86
; Sequence 86, Application US/10633850
; Publication NO. US20040205842A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; APPLICANT: Grunseem, Wilhelm
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633,850
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/135,004
; PRIOR FILING DATE: 1999-03-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 86
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-10-633-850-86

```

Query Match	77.4%;	Score 1500.5;	DB 17;	Length 352;
Best Local Similarity	75.9%;	Pred. No. 4.5e-126;		
Matches 267; Conservative	44;	Mismatches 40;	Indels 1;	Gaps 1;

```
Qy 1 MPP-PKKERVOSKNYFLTYPCSLSKREALSOLQNLNTPVNKKFKIKICREIHENGEPHL 59
Db 1 MPPHFKFQJNANKYFLTYPCSLSKREALSOLQNLNTPVNKKFKIKICREIHENGEPHL 60
Qy 60 VLVOPEGKYCTNNRFPDLVSPTRSAHFHPIIQAKSSDVKSYIDKDGDTIEWDFOID 119
Db 61 VLIOPEGKYCCQNRFPDLVSPTRSAHFHPIIQAKSSDVKTYIDKDGDTLVMGEFOVD 120
Qy 120 GRSARGGQOSANDSYAQLNAGSVQALAVIREQPDVLOHNHNSNLERIFAKAPER 179
Db 121 GRSARGGQOTSNDAAEALNASSKAAALQIIREKIPKYLFOFENLNSNLDRIFDKTEP 180
Qy 180 WVPFVOVSSFTNVDEMOMANDYFGTGDAPDPDPVSIIEGDSRTGKTMMARALGPHN 239
Db 181 WLPFHVSSFTNVDEMOMANDYFGKSSARPERPISIIIEGDSRTGKTMMARSLGPHN 240
Qy 240 YLSGHLDFNGRVFSNDVQYVNIIDIAPHYLLKMKKELLAGQKXQNSCKYKGPVQIKG 299
Db 241 YLSGHLDFNLSRVSNKVEYVNIIDVTPQYLKMKKELLAGQKXQNSCKYKGPVQIKG 300
Qy 300 IPATVLCNPGEGASYKFLDKAENTGLKNWTIKNAIFITLTAPLYQESTQAS 351
Db 301 IPSIVLCNPGEGASYKFLDKAENTPLKNWTFHNAKFVFLNSPLVQSTQSS 352
```

RESULT 15

```
US-10-613-850-82
; Sequence 82, Application US/10633850
; Publication No. US20040205843A1
; GENERAL INFORMATION:
; APPLICANT: Hanley-Bowdoin, Linda
; APPLICANT: Orozco, Beverly M.
; TITLE OF INVENTION: GEMINIVIRUS RESISTANT TRANSGENIC PLANTS
; FILE REFERENCE: 5051.4581P
; CURRENT APPLICATION NUMBER: US/10/633, 850
; PRIOR FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: US 09/289,346
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 60/125,004
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 82
; LENGTH: 352
; TYPE: PRT
; ORGANISM: Tomato golden mosaic virus
US-10-613-850-82
```

Query Match 77.3%; Score 1499.5; DB 17; Length 352;

Best Local Similarity 75.9%; Pred. No. 5.5e-126; Matches 267; Conservative 43; Mismatches 41; Indels 1; Gaps 1;

```
Qy 1 MPP-PKKERVOSKNYFLTYPCSLSKREALSOLQNLNTPVNKKFKIKICREIHENGEPHL 59
Db 1 MPPHFKFQJNANKYFLTYPCSLSKREALSOLQNLNTPVNKKFKIKICREIHENGEPHL 60
Qy 60 VLVOPEGKYCTNNRFPDLVSPTRSAHFHPIIQAKSSDVKSYIDKDGDTIEWDFOID 119
Db 61 VLIOPEGKYCCQNRFPDLVSPTRSAHFHPIIQAKSSDVKTYIDKDGDTLVMGEFOVD 120
Qy 120 GRSARGGQOSANDSYAQLNAGSVQALAVIREQPDVLOHNHNSNLERIFAKAPER 179
Db 121 GRSARGGQOTSNDAAEALNASSKAAALQIIREKIPKYLFOFENLNSNLDRIFDKTEP 180
Qy 180 WVPFVOVSSFTNVDEMOMANDYFGTGDAPDPDPVSIIEGDSRTGKTMMARALGPHN 239
Db 181 WLPFHVSSFTNVDEMOMANDYFGKSSARPERPISIIIEGDSRTGKTMMARSLGPHN 240
Qy 240 YLSGHLDFNGRVFSNDVQYVNIIDIAPHYLLKMKKELLAGQKXQNSCKYKGPVQIKG 299
Db 241 YLSGHLDFNLSRVSNKVEYVNIIDVTPQYLKMKKELLAGQKXQNSCKYKGPVQIKG 300
```

```
Qy 300 IPATVLCNPGEGASYKFLDKAENTGLKNWTIKNAIFITLTAPLYQESTQAS 351
Db 301 IPSIVLCNPGEGASYKFLDKAENTPLKNWTFHNAKFVFLNSPLVQSTQSS 352
```

Search completed: December 3, 2004, 15:13:08
Job time: 145 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2004, 14:57:49 ; Search time 48 Seconds
(without alignments)
723.630 Million cell updates/sec

Title: US-09-491-063A-2

Sequence: 1 MEPPKKFRVQSKNYFLTYPO.....PLYQSTQASQETGNQKAG 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1920	99.0	358	1 JQ1870	ALI protein - toma
2	1572	81.1	361	1 QOCVPT	ALI protein - pota
3	1562	80.6	355	1 QOCVW1	ALI protein - abut
4	1502.5	77.5	352	1 QOCVLI	ALI protein - toma
5	1344	69.3	385	2 S28360	ALI protein - beet
6	1340.5	69.1	362	1 JQ1887	ALI protein - toma
7	1338.5	69.0	349	2 JQ2300	replicase - pepper
8	1338.5	69.0	349	2 S31875	ALI protein - pepp
9	1311.5	67.6	359	2 S22593	hypothetical prote
10	1310.5	67.6	360	2 S59885	replication-associ
11	1307	67.4	351	2 JQ2327	ALI protein - indi
12	1305.5	67.3	359	2 S39211	Gene C1 protein -
13	1296.5	66.9	357	1 QOCVCI	ALI protein - toma
14	1290.5	66.6	359	2 S39235	gene C1 protein -
15	1282.5	66.1	358	2 S07594	hypothetical prote
16	1166.5	60.2	347	1 QOCVSI	ALI protein - equa
17	464.5	24.0	351	2 S49387	replication-associ
18	461.5	23.8	351	2 B24356	replication-associ
19	409.5	21.1	131	2 S45059	ALI protein (clone
20	268	13.8	411	1 QOCVPZ	PI polypeptide - m
21	254.5	13.9	217	2 JQ1358	C1 protein - misca
22	250	12.9	146	2 C42452	C1 protein - tobac
23	248	12.8	295	2 D42452	C1 protein - tobac
24	246	12.7	295	2 JU0043	hypothetical 33.2K
25	238	12.3	136	2 JQ1359	C2 protein - misca
26	202.5	10.4	272	2 A05158	hypothetical prote
27	199.5	10.3	141	2 JQ1553	C2 protein - panic
28	199.5	10.3	272	2 S04806	hypothetical prote
29	196.5	10.1	272	2 T10116	replication protei

30	191.5	9.9	153	2 T10115	replication-associ
31	188.5	9.7	148	2 S04807	hypothetical prote
32	187.5	9.7	136	2 JU0044	hypothetical 15.8K
33	177	9.1	333	2 JQ1552	C1 protein - panic
34	161.5	8.3	84	2 PS0142	replication-associ
35	105	5.4	979	2 T50956	hypothetical prote
36	102.5	5.3	562	1 UKHRT	t-plasminogen acti
37	102.5	5.3	1244	2 S73731	probable lipoprote
38	98.5	5.1	2116	2 A26655	myosin heavy chain
39	97	5.0	356	2 E81269	hypothetical prote
40	96.5	5.0	287	1 PMVKL	inorganic diphosph
41	96	5.0	421	2 AG2587	lytic murein trans
42	96	5.0	421	2 G97369	hypothetical prote
43	96	5.0	539	2 D83764	chitinase BHO916 l
44	96	5.0	1203	1 A47501	nitric-oxide synth
45	95	4.9	472	2 F86702	hypothetical prote

ALIGNMENTS

```
RESULT 1
JQ1870
ALI protein - tomato mottle virus (isolate Florida)
C/Species: tomato mottle virus
C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004
C/Accession: JQ1870
R/Abouzeid, A.M.; Polston, J.E.; Hiebert, E.
J. Gen. Virol. 73, 3225-3229, 1992
A/Title: The nucleotide sequence of tomato mottle virus, a new geminivirus isolated from
A/Reference number: JQ1869; NCBI:3107858; PMID:1469361
A/Accession: JQ1870
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-358 <ABO>
A/Cross-references: UNIPROT:Q06657; GB:L14460
C/Genetic:
A/Map position: segment A
C/Superfamily: tomato golden mosaic virus ALI protein

Query Match          99.0% Score 1920; DB 1; Length 358;
Best Local Similarity 100.0% Pred. No. 8.1e-141;
Matches 358; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 PKKFRVQSKNYFLTYPOCSLSKEALSQQLNTLPVKKRFIKICREIHENGEBHLVAVQ 63
DB 1 PKKFRVQSKNYFLTYPOCSLSKEALSQQLNTLPVKKRFIKICREIHENGEBHLVAVQ 60

QY 64 FEGRYQCTNNRFPDLVSPTRSAHFPHNIQAKSSDVKSYYIDQDGTIEKGDFOIDGRSA 123
DB 61 FEGRYQCTNNRFPDLVSPTRSAHFPHNIQAKSSDVKSYYIDQDGTIEKGDFOIDGRSA 120

QY 124 RGGQOSANDSYAKALNAGSVQSLAVLREOPDPFLQNNINRSLERIPAKAPEPVVP 183
DB 121 RGGQOSANDSYAKALNAGSVQSLAVLREOPDPFLQNNINRSLERIPAKAPEPVVP 180

QY 184 FOVSSFTNVPDEMGEWADNYFGTGAAPPDRPVSIIVEGDSRTQKTMWABALPHTLSG 243
DB 181 FOVSSFTNVPDEMGEWADNYFGTGAAPPDRPVSIIVEGDSRTQKTMWABALPHTLSG 240

QY 244 HLDPNGRVRSNDVQYVVIDIAHYIKLKKMKELLAGQKDWQSNCKYKGVQIKGIPAI 303
DB 241 HLDPNGRVRSNDVQYVVIDIAHYIKLKKMKELLAGQKDWQSNCKYKGVQIKGIPAI 300

QY 304 VLCNPGEGASYKFEFLKAEKNTGLKNTIKNAIFITLTAPLYQSTQASQETGNQKAG 361
DB 301 VLCNPGEGASYKFEFLKAEKNTGLKNTIKNAIFITLTAPLYQSTQASQETGNQKAG 358

RESULT 2
QOCVPT
ALI protein - potato yellow mosaic virus (isolate Venezuela)
C/Species: potato yellow mosaic virus
```

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C/Accession: J00364
R/Courtesy, R.H.A., Coffin, R.S., Roberts, E.J.F., Hamilton, W.D.O.
J. Gen. Virol. 72, 1515-1520, 1991
A/Title: The nucleotide sequence of the infectious cloned DNA components of potato yellow vein virus
A/Reference number: J00362; MUID:91311403; PMID:1856690
A/Accession: J00364
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 15361 <CCU>
A/Cross-references: UNIPROT:P27258; GB:D00940; NID:g222458; PIDD:BAA00782.1; PID:g222458
C/Genetics:
A/Map position: segment A
C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 81.1%; Score 1572; DB 1; Length 361;
Best Local Similarity 77.9%; Pred. No. 6.5e-114;
Matches 279; Conservative 39; Mismatches 40; Indels 0; Gaps 0;

QY 1 MPPPKFVQSKNYFLTYPQCSLSKEALSQLQNLNTPVKKFKIKICREIHENGEPHLY 60
Db 1 MPRKGSFSAKKNYFLTYPQCSLSKEALSQLQNLTPVKKFKIKICREIHENGEPHLY 60
QY 61 LVQEBGKQCTNNRPFDVSPTRSAHHPHNIQAKSSDVYSYIDKQDPTIEMGDPOIDG 120
Db 61 LVQEBGKQCTNNRPFDVSPTRSTHFPHPNIQAKSSDVYSYKQKGDPTIEMGLFOIDG 120
QY 121 RSAGGQGOQANDSYAKALNAGSVQALAVLREOPKCFVLQNHNIIRNLERIFAKAPEPW 180
Db 121 RSAGGQGOQTVNDAAEALNAGSTKEAMKIIKELPEKFLFOYHNLSCNDRIEFAKAPETW 180
QY 181 VPPQVSSFTNVPPDMQEMADNYFTGTDAPPPDPVSIYVEGDSRTGKTMMARALGPHNY 240
Db 181 APPPLSSFTVPDEMOMADNYGFGKSSAAPPERPISIIIEGDSRRKTMARVLAGPHNY 240
QY 241 LSGHLDFEGRVFSNDVOYNNVDDIAPHYLLKLLKHWKELLGAQKQMSCKYKQPKVQIKGI 300
Db 241 LSGHLDFEGRVFSNEVENNVDDVAPQYLKLLKHWKELLGAQRDQMSCKYKQPKVQIKGI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWITIKNAIFITTLAPLYQESTQASQETGNOK 358
Db 301 PSIVLCNPGEGSSYKAFLDKDNASTLKNWITIKNAVFIITTPALYQEGTQASKEGNGE 358

RESULT 3
QOCVNI
AV1 protein - abutilon mosaic virus (isolate west India)
C/Species: abutilon mosaic virus
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
C/Accession: A36214
R/Frischmuth, T.; Zimmat, G.; Jeske, H.
VIROLOGY 178, 461-468, 1990
A/Title: The nucleotide sequence of the abutilon mosaic virus reveals prokaryotic as well
A/Reference number: A36214; MUID:91020984; PMID:2219703
A/Accession: A36214
A/Molecule type: DNA
A/Residues: 1-355 <FRI>
A/Cross-references: UNIPROT:P21947; EMBL:X15983
C/Genetics:
A/Map position: segment A
C/Superfamily: tomato golden mosaic virus AV1 protein

Query Match 80.6%; Score 1562; DB 1; Length 355;
Best Local Similarity 81.4%; Pred. No. 3.8e-113;
Matches 293; Conservative 22; Mismatches 35; Indels 10; Gaps 3;

QY 1 MPPPKFVQSKNYFLTYPQCSLSKEALSQLQNLNTPVKKFKIKICREIHENGEPHLY 60
Db 1 MPPPKFVQAKNYFLTYPQCSLTKEALSQLQNLNTPVNNKFKIKICREIHENGEPHLY 60
QY 61 LVQEBGKQCTNNRPFDVSPTRSAHHPHNIQAKSSDVYSYIDKQDPTIEMGDPOIDG 120
Db 61 LVQEBGKQCTNNRPFDVSPTRSAHHPHNIQAKSSDVYSYIDKQDPTIEMGEFOIDG 120

```

QY 121 RSARGGQGSANDSVAKALNAGVQSALAVLREOPDPFLQNNHINSNLERIPAKAPEPW 180
Db 121 RSARGGQGTANDSVAKALNAGDVQSALNLIKKEQPDVYLQNNHINSNLERIPAKAPEPW 180
QY 181 VPPFGVSSFTNVPEDEMQEWADNYFETGDAAP--PDRPVSIIVEGDSRTGKTMARALGPH 238
Db 181 VAGFSPSLRPPRRRCRSGRMILG---VPLRPDRPPLSLIVEGDSRTGKTMARALGPH 237
QY 229 NYLSGHLDPNGVSPENDQVYNIIDLIAPHYLKIKHMKELLGAQKMDQSNCKYKPVQIKG 298
Db 228 NYLSGHLDPNGVSYNEVNEYNIIDVAPHYLKLKHMKELLGAQKMDQSNCKLAKPVQIKG 297
QY 299 GIPATVLCNPGGASGYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTQASQETGNOK 358
Db 298 GIRATVLCNPGGSSGYKEFLDKENRGLRNWTLKNAIFITLTAPLYQ-----GRHTGRPR 352

RESULT 4
OOCVLI
A11 protein - tomato golden mosaic virus
C:Species: tomato golden mosaic virus
A:Note: host Nicotiana sp. (tobacco)
C:Date: 28-Aug-1985 #sequence_revision 28-Aug-1985 #text_change 09-Jul-2004
C:Accession: A04170
R:Hamilton, W.D.O.; Stein, V.E.; Coutter, R.H.A.; Buck, K.W.
A>Title: Complete nucleotide sequence of the infectious cloned DNA components of tomato
A:Reference number: A04163
A:Accession: A04170
A:Molecule type: DNA
A:Residues: 1-352 <HAM>
A:Cross-references: UNIPROT:P03567
C:Comment: The genome consists of two circular, single-stranded DNA components, DNA A and
C:Genetics:
A:Map position: segment A
C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 77.5%; Score 1502.5; DB 1; Length 352;
Beet Local Similarity 75.9%; Pred No. 1.5e-108;
Matches 267; Conservative 44; Mismatches 40; Indels 1; Gaps 1;

QY 1 MPP-PKPRVQSVKSNFLTYPOCSLKEALSQLQNLNTPVKKKFIKICRELHENGEBEHL 59
Db 1 MSHHKRPFQINKNFILTYPOCSLKEESLSQLQNLNTPINKKFKIKICRELHEDGQPHL 60
QY 60 VLVOEGKQCTNNRPFDLVSPTRSAHFHPNIOGAASSSVKSYIDKDGPTIEMGDPQID 119
Db 61 VLIOEGKKCCNORFDLVSPTRSAHFHPNIOGASSSDVKTYIDKDGTLVWGEPOVD 120
QY 120 GNSAAGGQGSANDSVAKALNAGSVQSALAVLREOPKDPFLQNNHINSNLERIFAKAPEP 179
Db 121 GNSAAGGCOTSDAAAEALNAGSKERALQIIRKIKIEKYLFGHNLSNLDRIFDKPIEP 180
QY 180 WVPFQVSSFTNVPEDEMQEWADNYFETGDAAPDRPVSIIIEGDSRTGKTMARALGPHN 239
Db 181 WLPFHVSSFTNVPEDEMQEWAEYFPGKSSAARPERPISIIIEGDSRTGKTMARSLGPHN 240
QY 240 YLSGHLDPNGRFPNDVQYNIIDLIAPHYLKIKHMKELLGAQKMDQSNCKYKPVQIKG 299
Db 241 YLSGHLDLNSRYNSKNVEYNIIDVTPQYLKIKHMKELLGAQKMDQSNCKYKPVQIKG 300
QY 300 IPATVLCNPGGASGYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTQAS 351
Db 301 IPSITVLCNPGGASGYKFLDKENRGLRNWTLKNAIFITLTAPLYQESTQSS 352

RESULT 5
A11 protein - beet curly top virus
C:Species: beet curly top virus
C:Date: 07-May-1993 #sequence_revision 07-May-1993 #text_change 09-Jul-2004

```


A:Molecule type: DNA
A:Residues: 1-349 <OR>
A/Cross-references: UNIPROT:Q06923; EMBL:X70418; NID:961023; PIDN:CAA49856.1; PID:961025
A/Note: the source is designated as pepper huasteco virus
C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 69.0%; Score 1338.5; DB 2; Length 349;
Best Local Similarity 67.9%; Pred. No. 7e-96;
Matches 239; Conservative 53; Mismatches 55; Indels 5; Gaps 3;

QY 1 MPPPKKFRVOSKNYFLTYPCSLSKERALSQLOLNTPVNKKFKIKICREIHENGEPHLHY 60
DB 1 MPPPKKFRVOSKNYFLTYPCSLSKERALSQLOLNTPVNKKFKIKICREIHENGEPHLHY 60
QY 61 LVQFEGKYOCNTNRFPDLVSPTRSAHPHPIQAKSSSDVKSYIDKGDITWEGDFQIDG 120
DB 61 LVQFEGKYOCNTNRFPDLVSPTRSAHPHPIQAKSSSDVKSYIDKGDITWEGDFQIDG 120
QY 121 RSARGGQOSANDSYAKALNAGVOSALAVREBPQDFVLQNNHNSLIERIFAKAPEPW 180
DB 121 RSARGGQOSANDSYAKALNAGVOSALAVREBPQDFVLQNNHNSLIERIFAKAPEPW 180
QY 181 VPPFQVSSFTNVDEQEW-ADNYFGTGAAPPDRPVSIIVEGDSRTGKTWAPALGPHN 239
DB 181 VPPFQVSSFTNVDEQEW-ADNYFGTGAAPPDRPVSIIVEGDSRTGKTWAPALGPHN 239
QY 240 YLSGHLDFNGRVESNDQVNVVIDIAHYLKLKHWKELLGAQKQWQSNCKYGRKPVQIKG 239
DB 239 YLSGHLDFNGRVESNDQVNVVIDIAHYLKLKHWKELLGAQKQWQSNCKYGRKPVQIKG 239
QY 300 IPAIVLCNPEGASYKEFLDKAENTGKKNWTIKNAIFITLTAPLYESTOAS 351
DB 297 IPTIFLCNPEGSSYKDYVSEKNSRLNDVQKNALVITIEALFTTGSGTSS 348

RESULT 9

S22593
hypothetical protein C4 - tomato yellow leaf curl virus
C/Species: tomato yellow leaf curl virus
C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C/Accession: S22593
R/Key: Pour, A.; Bendahmane, M.; Matzeit, V.; Accotto, G.P.; Crepsl, S.; Gronenborn, B.
Nucleic Acids Res. 19, 6763-6769, 1991
A/Title: Tomato yellow leaf curl virus from Sardinia is a whitefly-transmitted monopartite
A/Reference number: S22588; MUID:92107660; PMID:1840676
A/Accession: S22593
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-359 <RHE>
A/Cross-references: UNIPROT:P27260; EMBL:X61153; NID:962211; PIDN:CAA43466.1; PID:962217
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1991
C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 67.6%; Score 1311.5; DB 2; Length 359;
Best Local Similarity 66.3%; Pred. No. 8.9e-94;
Matches 240; Conservative 48; Mismatches 65; Indels 9; Gaps 4;

QY 1 MPPPKKFRVOSKNYFLTYPCSLSKERALSQLOLNTPVNKKFKIKICREIHENGEPHLHY 60
DB 1 MPPPKKFRVOSKNYFLTYPCSLSKERALSQLOLNTPVNKKFKIKICREIHENGEPHLHY 60
QY 61 LVQFEGKYOCNTNRFPDLVSPTRSAHPHPIQAKSSSDVKSYIDKGDITWEGDFQIDG 120
DB 61 LVQFEGKYOCNTNRFPDLVSPTRSAHPHPIQAKSSSDVKSYIDKGDITWEGDFQIDG 120
QY 121 RSARGGQOSANDSYAKALNAGVOSALAVREBPQDFVLQNNHNSLIERIFAKAPEPW 180
DB 121 RSARGGQOSANDSYAKALNAGVOSALAVREBPQDFVLQNNHNSLIERIFAKAPEPW 180
QY 181 VPPFQVSSFTNVDEQEW-ADNYFGTGAAPPDRPVSIIVEGDSRTGKTWAPALGPHN 239
DB 181 VPPFQVSSFTNVDEQEW-ADNYFGTGAAPPDRPVSIIVEGDSRTGKTWAPALGPHN 239

QY 240 YLSGHLDFNGRVESNDQVNVVIDIAHYLKLKHWKELLGAQKQWQSNCKYGRKPVQIKG 239
DB 239 YLSGHLDFNGRVESNDQVNVVIDIAHYLKLKHWKELLGAQKQWQSNCKYGRKPVQIKG 239
QY 300 IPAIVLCNPEGASYKEFLDKAENTGKKNWTIKNAIFITLTAPLYESTOAS 351
DB 297 IPTIFLCNPEGSSYKDYVSEKNSRLNDVQKNALVITIEALFTTGSGTSS 348

QY 356 NQ 357
DB 357 SE 358

RESULT 10

S59885
replication-associated protein C1 - tomato yellow leaf curl virus
C/Species: tomato yellow leaf curl virus
C/Date: 14-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C/Accession: S59885
R/Hong, Y.; Harrison, B.D.
submitted to the EMBL Data Library, February 1995
A/Description: Nucleotide sequences from tomato leaf curl viruses from different countries
d geminiviruses.
A/Reference number: S59885
A/Accession: S59885
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-360 <HON>
A/Cross-references: UNIPROT:Q88557; EMBL:Z48182; NID:9944838; PIDN:CAA88229.1; PID:997423
C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 67.6%; Score 1310.5; DB 2; Length 360;
Best Local Similarity 67.6%; Pred. No. 1.1e-93;
Matches 244; Conservative 46; Mismatches 62; Indels 9; Gaps 4;

QY 1 MPPPKKFRVOSKNYFLTYPCSLSKERALSQLOLNTPVNKKFKIKICREIHENGEPHLHY 60
DB 1 MPPPKKFRVOSKNYFLTYPCSLSKERALSQLOLNTPVNKKFKIKICREIHENGEPHLHY 60
QY 61 LVQFEGKYOCNTNRFPDLVSPTRSAHPHPIQAKSSSDVKSYIDKGDITWEGDFQIDG 120
DB 61 LVQFEGKYOCNTNRFPDLVSPTRSAHPHPIQAKSSSDVKSYIDKGDITWEGDFQIDG 120
QY 121 RSARGGQOSANDSYAKALNAGVOSALAVREBPQDFVLQNNHNSLIERIFAKAPEPW 180
DB 121 RSARGGQOSANDSYAKALNAGVOSALAVREBPQDFVLQNNHNSLIERIFAKAPEPW 180
QY 181 VPPFQVSSFTNVDEQEW-ADNYFGTGAAPPDRPVSIIVEGDSRTGKTWAPALGPHN 240
DB 181 VPPFQVSSFTNVDEQEW-ADNYFGTGAAPPDRPVSIIVEGDSRTGKTWAPALGPHN 240
QY 241 LSGHLDFNGRVESNDQVNVVIDIAHYLKLKHWKELLGAQKQWQSNCKYGRKPVQIKG 300
DB 239 LSGHLDFNGRVESNDQVNVVIDIAHYLKLKHWKELLGAQKQWQSNCKYGRKPVQIKG 296
QY 301 IPAIVLCNPEGASYKEFLDKAENTGKKNWTIKNAIFITLTAPLYESTOAS 356
DB 297 IPTIFLCNPEGSSYKDYVSEKNSRLNDVQKNALVITIEALFTTGSGTSS 348

RESULT 11

JQ2327
AL1 protein - Indian cassava mosaic virus
N/Alternate names: replication-associated protein
C/Species: Indian cassava mosaic virus
C/Date: 28-Aug-1985 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C/Accession: JQ2327; S35883
R/Hong, Y.G.; Robinson, D.J.; Harrison, B.D.
J. Gen. Virol. 74, 2437-2443, 1993

A/Title: Nucleotide sequence evidence for the occurrence of three distinct whitefly-transmitted virus isolates from tomato golden mosaic virus (TGMV) isolates from the
 A/Reference number: JQ2326; MID:94065670; PMID:8245859
 A/Accession: JQ2326
 A/Molecule type: DNA
 A/Residues: 1-351 <HON>
 A/Cross-references: UNIPROT:Q82676; EMBL:Z24758; NID:g395351; PIDD:CAA80891.1; PID:g5840
 C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 67.4%; Score 1307; DB 2; Length 351;

Best Local Similarity 67.6%; Pred. No. 1.9e-93;
 Matches 240; Conservative 43; Mismatches 66; Indels 6; Gaps 3;

QY 1 MPPKPKRVQSNKYFLTYPCSLSKKEBALSOLOLNTLVNPKKFKIKICREHENGEPHLAV 60
 DB 1 MSPKRFQIAKAKYFLTYPCSLSKKEBALSOLOLNTLVNPKKFKIKICREHENGEPHLAV 60
 QY 61 LVPEKGYOCTNNRFPDLVSPTRSAHPHPIOGAKSSSDVKSYYIDKDGDTIEMGDFQIDG 120
 DB 61 LVPEKGYOCTNNRFPDLVSPTRSAHPHPIOGAKSSSDVKSYYIDKDGDTIEMGDFQIDG 120
 QY 121 RSARGGQGSANDSYAKALNAGVOSALAVREBPDPVLOHNHINSNLERIFAKAPEPW 180
 DB 121 RSARGGQGSANDSYAKALNAGVOSALAVREBPDPVLOHNHINSNLERIFAKAPEPW 180
 QY 121 RSARGGQGSANDSYAKALNAGVOSALAVREBPDPVLOHNHINSNLERIFAKAPEPW 180
 DB 121 RSARGGQGSANDSYAKALNAGVOSALAVREBPDPVLOHNHINSNLERIFAKAPEPW 180
 QY 181 VPPFQVSSFTNVDEMOEW-ADNYFGTGDAAPDPDPVSIIVEGDSRTGKTMMARALGPHN 239
 DB 181 ENFPFSSFDVPEELEDWFEHENVMG--RARPRLPKSIYIEGDSRTGKTMMARALGPHN 237
 QY 240 YLSGHLDFNGRVSNDOVNVIDIAPIHYLKLKMKKELLGAQKQWQSNCKYKGPVOIKGG 239
 DB 238 YLGGHLDLSQKXVSNNAWNVNIDVDVPHY--LKHFKIHFSGPEWQSNCKYKGPVOIKGG 235
 QY 300 IPAIVLCNPEGASVKEFLDKAENTGLKNMTIKNAIFITLTAPLYOBSTOASOET 354
 DB 296 IPTITLCNPEGASVKEFLDKAENTGLKNMTIKNAIFITLTAPLYOBSTOASOET 350

RESULT 12

gene C1 protein - tomato yellow leaf curl virus

C/Species: tomato yellow leaf curl virus
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C/Accession: S39211

R/Norris, E.; Hidalgo, E.; Accotto, G.; Moriones, E.
 submitted to the EMBL Data Library, August 1993
 A/Description: High similarity among the tomato yellow leaf curl virus isolates from the

A/Reference number: S39209
 A/Accession: S39211
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-359 <NOR>
 A/Cross-references: UNIPROT:P38609; EMBL:Z25751; NID:g433655; PIDD:CAA81026.1; PID:g4336

C/Superfamily: tomato golden mosaic virus AL1 protein
 Query Match 67.3%; Score 1305.5; DB 2; Length 359;
 Best Local Similarity 67.1%; Pred. No. 2.6e-93;
 Matches 235; Conservative 52; Mismatches 58; Indels 5; Gaps 3;

QY 1 MPPKPKRVQSNKYFLTYPCSLSKKEBALSOLOLNTLVNPKKFKIKICREHENGEPHLAV 60
 DB 1 MAOPKRFQIAKAKYFLTYPCSLSKKEBALSOLOLNTLVNPKKFKIKICREHENGEPHLAV 60
 QY 61 LVPEKGYOCTNNRFPDLVSPTRSAHPHPIOGAKSSSDVKSYYIDKDGDTIEMGDFQIDG 120
 DB 61 LVPEKGYOCTNNRFPDLVSPTRSAHPHPIOGAKSSSDVKSYYIDKDGDTIEMGDFQIDG 120
 QY 121 RSARGGQGSANDSYAKALNAGVOSALAVREBPDPVLOHNHINSNLERIFAKAPEPW 180
 DB 121 RSARGGQGSANDSYAKALNAGVOSALAVREBPDPVLOHNHINSNLERIFAKAPEPW 180
 QY 181 VPPFQVSSFTNVDEMOEW-ADNYFGTGDAAPDPDPVSIIVEGDSRTGKTMMARALGPHN 239
 DB 181 VPPFQVSSFTNVDEMOEW-ADNYFGTGDAAPDPDPVSIIVEGDSRTGKTMMARALGPHN 238

QY 240 YLSGHLDFNGRVSNDOVNVIDIAPIHYLKLKMKKELLGAQKQWQSNCKYKGPVOIKGG 239
 DB 238 YLGGHLDLSQKXVSNNAWNVNIDVDVPHY--LKHFKIHFSGPEWQSNCKYKGPVOIKGG 236
 QY 300 IPAIVLCNPEGASVKEFLDKAENTGLKNMTIKNAIFITLTAPLYOBSTOASOET 354
 DB 297 IPTITLCNPEGASVKEFLDKAENTGLKNMTIKNAIFITLTAPLYOBSTOASOET 346

RESULT 13

AL1 protein - tomato yellow leaf curl virus

N/Alternate names: C1 protein
 C/Species: tomato yellow leaf curl virus
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C/Accession: D40779

R/Navot, N.; Pichereky, E.; Zeidan, M.; Zandir, D.; Cosmek, H.
 Virology 185, 151-161, 1991
 A/Title: Tomato yellow leaf curl virus: a whitefly-transmitted geminivirus with a single

A/Reference number: A40779; MID:92024070; PMID:1926771
 A/Accession: D40779
 A/Status: translation not shown
 A/Molecule type: DNA
 A/Residues: 1-357 <NAV>
 A/Cross-references: UNIPROT:P27259; GB:X15656; NID:g62204; PIDD:CAA33688.1; PID:g62207
 C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 66.9%; Score 1296.5; DB 1; Length 357;

Best Local Similarity 66.6%; Pred. No. 1.3e-92;
 Matches 239; Conservative 52; Mismatches 59; Indels 9; Gaps 4;

QY 4 PKKRVQSNKYFLTYPCSLSKKEBALSOLOLNTLVNPKKFKIKICREHENGEPHLAV 63
 DB 2 PRFKIYAKNVFLTYPCSLSKKEBALSOLOLNTLVNPKKFKIKICREHENGEPHLAV 61
 QY 64 FEKGYOCTNNRFPDLVSPTRSAHPHPIOGAKSSSDVKSYYIDKDGDTIEMGDFQIDG 123
 DB 62 FEKGYOCTNNRFPDLVSPTRSAHPHPIOGAKSSSDVKSYYIDKDGDTIEMGDFQIDG 121
 QY 124 RGGQGSANDSYAKALNAGVOSALAVREBPDPVLOHNHINSNLERIFAKAPEPW 183
 DB 122 RGGQGSANDSYAKALNAGVOSALAVREBPDPVLOHNHINSNLERIFAKAPEPW 181
 QY 184 FQVSEFTNVDEMOEW-ADNYFGTGDAAPDPDPVSIIVEGDSRTGKTMMARALGPHN 239
 DB 182 FLSSSTNVQVDELEWVAENV--VSAAPBWRISIVIEGDSRTGKTMMARALGPHN 239
 QY 243 GHIDFNGRVSNDOVNVIDIAPIHYLKLKMKKELLGAQKQWQSNCKYKGPVOIKG 302
 DB 240 GHIDFNGRVSNDOVNVIDIAPIHYLKLKMKKELLGAQKQWQSNCKYKGPVOIKG 297
 QY 303 IYLCNPEGASVKEFLDKAENTGLKNMTIKNAIFITLTAPLYOBSTOASOET 357
 DB 298 IFLCNPEGASVKEFLDKAENTGLKNMTIKNAIFITLTAPLYOBSTOASOET 356

RESULT 14

gene C1 protein - tomato yellow leaf curl virus

C/Species: tomato yellow leaf curl virus
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
 C/Accession: S39235

R/Crespi, S.; Norris, E.; Valira, A.; Bosco, D.; Accotto, G.
 submitted to the EMBL Data Library, December 1993
 A/Description: A cloned DNA from a TYLCV isolate from Sicily showing low infectivity.

A/Reference number: S39233
 A/Accession: S39235
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-359 <CRE>
 A/Cross-references: UNIPROT:Q88949; EMBL:Z28390; NID:g1041671; PID:g1334964
 C/Superfamily: tomato golden mosaic virus AL1 protein

Query Match 66.6%; Score 1290.5; DB 2; Length 359;
 Best Local Similarity 64.5%; Pred. No. 3.7e-92;
 Matches 234; Conservative 56; Mismatches 64; Indels 9; Gaps 4;

```

QY 1 MPPKFERVOSKNVFLTYPOCSLSKEBALSQLQNTLPVKKFKIKICREIHENGEPHIAV 60
DB 1 MAGPKRQINAKHYFLTFPPKCCULKEALBQLLQFTPNKKYIKICREIHEDGQPLHI 60
QY 61 LVQPEGKYQCTNNRFFFLVSPTRSAHFHPIIQAKSSDVKSYIDKQDPTIEMCDFQIDG 120
DB 61 LMOFEGKFNCKNNRFFFLVSPTRSAHFHPIIQAKSSDVKSYIDKQDPTIEMCFQIDG 120
QY 121 RSARGGQSSANDSYAKALNAGVQSALAVLREBQPKDFVLQNHNRISNLERIFAKAPEPW 180
DB 121 RSARGGQITNDAYAKALNARSKEALDVIKQLAPRDYVLFHFNISNLDKFOVPAPY 180
QY 181 VPPFOVSSFTNVDPDEMEW-ADNYFGTDAAAPPDPVSIIVEGDSRTGKTMMARALGPHN 239
DB 181 VSPFLSSFDQVPELEHWTSENMDV--AARPRPVSIVIEGDSRTGKTMMARSLGPHN 238
QY 240 YLSGHLDPNGRVSNVDQVNVIDIAHYTLKHKMKELGAQKDQWQSNCKYKQVQIKGG 299
DB 239 YLGGHLDLSQKVSNNAMVNVIDVDPHY--LKIFKEFMGAQRDMQNTYKQKPIQIKGG 296
QY 300 IPAIVLCNPGEGASYKEFLDKAENTGLKNWTKNAIFITLTAPLY---QESTQASQETG 355
DB 297 IFTIFLCNPGPOSSFKEYLDBEKKQALKNNAVKNAIFVTIDQPLFTDHQNTTPHROEA 356
QY 356 NQK 358
DB 357 GEE 359

```

RESULT 15

S07594
 hypothetical protein, 40.4K - cassava latent virus (Nigerian isolate)
 C:Species: cassava latent virus
 C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C:Accession: S07594
 R:Morris, B.; Coates, L.; Lowe, S.; Richardson, K.; Eddy, P.
 Nucleic Acids Res. 18, 197-198, 1990
 A:Title: Nucleotide sequence of the infectious cloned DNA components of African cassava
 A:Reference number: S07590; MUID:90174930; PMID:2308831
 A:Accession: S07594
 A:Status: translation not shown
 A:Molecule type: DNA
 A:Residues: 1-358 <MOR>
 A:Cross-references: UNIPROT:P14972; EMBL:X17095; NID:G59371; PIDN:CAA34953.1; PID:G59376
 C:Genetic:
 A:Map position: segment DNA1
 C:Superfamily: tomato golden mosaic virus A11 protein

Query Match 66.1%; Score 1282.5; DB 2; Length 358;
 Best Local Similarity 68.6%; Pred. No. 1.6e-91;
 Matches 240; Conservative 38; Mismatches 67; Indels 5; Gaps 3;

```

QY 6 KFRVQSNVFLTYPOCSLSKEBALSQLQNTLPVKKFKIKICREIHENGEPHIAVQFE 65
DB 5 RFRVQANVFLTYPNCISIPKHLISFTQISLPENPKFIKICREIHONGEPHIALIQFE 64
QY 66 GKVOCTNNRFFFDLVSPTRSAHFHPIIQAKSSDVKSYIDKQDPTIEMGDFQIDGRSARG 125
DB 65 GKTTITNNRFLPDCVHPSCSTNHFHPIIQAKSSDVKSYIDKQDPTIEMGQFQIDGRSARG 124
QY 126 GQGSANDSYAKALNAGVQSALAVLREBQPKDFVLQNHNRISNLERIFAKAPEWVPPFQ 185
DB 125 GQGSANDAYAKALNSGSKSEALNVRELVPKDFVLQFNHNSNLDRIQEPAPVYVSPFP 184
QY 186 VSPFTNVDPDEMEW-ADNYFGTDAAAPPDPVSIIVEGDSRTGKTMMARALGPHNYLSGH 244
DB 185 CSSFDQVPELEHWTSENMDV--RDSAPRMPRPNISIVIEGDSRTGKTIVARSIGPHNYLGGH 242

```

```

QY 245 LDFNGRVFSNDVQVNVIDIAHYTLKHKMKELGAQKDQWQSNCKYKQVQIKGGIPIAV 304
DB 243 LDISPKVFTNDAMVNVIDVDPHY--LKIFKEFMGSQRDMQNTYKQKPIQIKGIPITIF 300
QY 305 LCNPGEGASYKEFLDKAENTGLKNWTKNAIFITLTAPLYQESTQASQET 354
DB 301 LCNPGFTSSYKEFLDEKQKALKNMALKNALFITLTPFLYSGSNOSQET 350

```

Search completed: December 3, 2004, 15:01:43
 Job time : 50 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 3, 2004, 14:55:20 ; Search time 193 Seconds

(Without alignments)
1076.219 Million cell updates/sec

Title: US-09-491-063a-2

Sequence: 1 MPPPKFRVQSKNYFLTYPO.....PLYQESTQASQETGNKQAG 361

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : UniProt 02: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1939	100.0	361	1 VAL1 TMOV	O06657 tomato mott
2	1908	98.4	361	2 Q67614	Q67614 tomato mott
3	1792	92.4	361	2 Q71963	Q71963 sida golden
4	1764	91.0	356	2 O11842	O11842 abutilon mo
5	1736	89.5	361	2 Q9YL74	Q9YL74 chino del t
6	1731	89.3	361	2 Q7HTH9	Q7HTH9 tomato mott
7	1722	88.8	361	2 Q36624	Q36624 tomato mott
8	1715	88.4	361	2 Q9J051	Q9J051 chino del t
9	1711	88.2	361	2 Q96612	Q96612 abutilon mo
10	1710	88.2	361	2 Q9J049	Q9J049 chino del t
11	1690	87.2	361	2 P89127	P89127 sida yellow
12	1689	87.1	361	2 Q8J1V1	Q8J1V1 tobacco lea
13	1664	85.8	361	2 Q67558	Q67558 bean dwarf
14	1652	85.2	350	2 Q71205	Q71205 potato yell
15	1640	84.6	361	2 P89122	P89122 sida golden
16	1635.5	84.3	360	2 Q9YVW9	Q9YVW9 sida golden
17	1606	82.8	358	2 Q91201	Q91201 tomato mosa
18	1597.5	82.4	360	2 Q9YVW5	Q9YVW5 sida golden
19	1596	82.4	348	2 Q911W5	Q911W5 macroptiliu
20	1585	81.7	353	2 Q9QGH3	Q9QGH3 bean golden
21	1582	81.6	353	2 Q80P44	Q80P44 bean golden
22	1575	81.2	353	2 P87726	P87726 bean golden
23	1572	81.1	353	2 Q01731	Q01731 bean golden
24	1572	81.1	361	2 VAL1 PYWV	P27258 potato yell
25	1569	80.9	351	2 Q41339	Q41339 potato yell
26	1566	80.8	361	2 Q8JW44	Q8JW44 potato yell
27	1562	80.6	355	1 VAL1 ABWV	P21947 abutilon mo
28	1557.5	80.3	351	2 Q7B8V7	Q7B8V7 sida golden
29	1549	79.9	351	2 Q9Q9R3	Q9Q9R3 dicliptera
30	1547	79.8	353	1 VAL1 BGVV	P51175 bean golden
31	1527	78.8	351	2 Q8QR22	Q8QR22 tomato chlo

32	1523	78.5	351	2 Q801H6	Q801H6 dicliptera
33	1522	78.5	358	2 Q70PB5	Q70PB5 sida micran
34	1522	78.5	358	2 CAD89709	CAD89709 sida micr
35	1516	78.2	358	2 Q6R7R5	Q6R7R5 tomato mosa
36	1516	78.2	358	2 AAR95968	AAR95968 tomato mo
37	1512	78.0	344	2 Q6R7Q8	Q6R7Q8 tomato yell
38	1512	78.0	344	2 AAR95975	AAR95975 tomato ye
39	1502.5	77.5	352	1 VAL1 TGMV	P03567 tomato gold
40	1498	77.3	361	2 Q67574	Q67574 bean golden
41	1497.5	77.2	349	2 Q8JUN1	Q8JUN1 macroptiliu
42	1493	77.0	346	2 Q7TSV0	Q7TSV0 tomato chin
43	1489.5	76.8	352	2 Q8QW66	Q8QW66 tomato chlo
44	1483	76.5	352	2 Q9E0C0	Q9E0C0 tomato rugo
45	1470	75.8	358	2 Q70PC0	Q70PC0 sida micran

ALIGNMENTS

```

RESULT 1
VAL1 TMOV          STANDARD;          PRT;          361 AA.
AC 006657;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE AL1 protein.
GN Name=AL1;
OS Tomato mottle virus (isolate Florida) (TMOV).
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=36449;
RN [1]
RP MEDLINE=93107858; PubMed=1469361;
RX Abouaid A.M., Polston J.E., Hiebert B.;
RT "The nucleotide sequence of tomato mottle virus, a new geminivirus
RT isolated from tomatoes in Florida."
RL J. Gen. Virol. 73:3225-3229(1992).
CC -I- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@sib-sib.ch).
CC -----
CC EMBL: L14460; AAC32414.1; -.
CC PIR: JQ1870; JQ1870.
CC HSSP: P27260; 1L51.
CC InterPro: IPR001191; Gemin1 AL1.
CC InterPro: IPR001301; Gemin1 AL1_CTV.
CC Pfam: PF00799; Gemin1 AL1_1.
CC PRINTS: PR00227; GEMCOATL1.
CC DR PRODOM: PD00228; GEMCOATL1.
CC DR PRODOM: PD000736; Gemin1_AL1_1.
CC KX ATP-Binding.
CC NP BIND: 222
CC SQ SEQUENCE 361 AA; 40516 MW; 813865CCEAC6950 CRC64;
Query Match 100.0%; Score 1939; DB 1; Length 361;
Best Local Similarity 100.0%; Pred. No. 4,5e-143;
Matches 361; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MPPPKFRVQSKNYFLTYPOCSLSKEEALSQLONTLPVKKRIRIKRELEHNGEPHLV 60
DB 1 MPPPKFRVQSKNYFLTYPOCSLSKEEALSQLONTLPVKKRIRIKRELEHNGEPHLV 60
QY 61 LVQFEGKYCTNNRFPDLVSPTRSAHFHNP1QGAKSSDVKSYIDKDGPTIEMGDFQIDG 120
DB 61 LVQFEGKYCTNNRFPDLVSPTRSAHFHNP1QGAKSSDVKSYIDKDGPTIEMGDFQIDG 120

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```

QY 121 RSARGGQOSANDSYAKALNAGSVOSALAVLREEQPKDFVLQNNHNRSLERIFAKAPEPW 180
|
|
|
Db 121 RSARGGQOSANDSYAKALNAGSVOSALAVLREEQPKDFVLQNNHNRSLERIFAKAPEPW 180
|
|
|
QY 181 VPPFQVSSFTNVPEDEQEMADNYFGTGDAAAPDRPVSIIYEGDSRTGKTMMARALGPHNY 240
|
|
|
Db 181 VPPFQVSSFTNVPEDEQEMADNYFGTGDAAAPDRPVSIIYEGDSRTGKTMMARALGPHNY 240
|
|
|
QY 241 LSGHLDNPGRVFNSNDVQYNYIDIDIAPHYLLKHKMKELLAGQKQWQSNCKTGKPVQIKGI 300
|
|
|
Db 241 LSGHLDNPGRVFNSNDVQYNYIDIDIAPHYLLKHKMKELLAGQKQWQSNCKTGKPVQIKGI 300
|
|
|
QY 301 PAIVLCNPGEGASKEFLDRAENTGLKNWTKKNAIFITLTPAPLYOESTQASOETGNQKQ 360
|
|
|
Db 301 PAIVLCNPGEGASKEFLDRAENTGLKNWTKKNAIFITLTPAPLYOESTQASOETGNQKQ 360
|
|
|
QY 361 G 361
|
|
|
Db 361 G 361

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RESULT 2

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ID Q67614 PRELIMINARY; PRT; 361 AA.
AC Q67614;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Replicative protein.
GN Name=AL1;
OS Tomato mottle virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_Taxid=10835;
RN [1]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Hidayat S.H., Rojas M.R., Maxwell D.P.;
RT "Infectious DNA clones of a new geminivirus associated with tomatoes in Florida."
RL Phytopathology 81:1184-1184(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9319780; PubMed=8423448;
RA Gilbertson R.L., Hidayat S.H., Paplomatas E.J., Rojas M.R., Hou Y.M., Maxwell D.P.;
RT "Pseudorecombination between infectious cloned DNA components of tomato mottle and bean dwarf mosaic geminiviruses."
RL J. Gen. Virol. 74:23-31(1993).
CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
DR EMBL; M90495; AAA02942.1; -.
DR HSSP; P27260; 1L5I.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001191; Gemin1 AL1.
DR InterPro; IPR001301; Gemin1 AL1_CLV.
DR Pfam; PF00799; Gemin1 AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR PRINTS; PR00228; GEMCOATL1.
DR ProDom; PD000736; Gemin1 AL1; 1.
SQ SEQUENCE 361 AA; 40547 MW; 3B3B2F75099A293C CRC64;

```

Query Match 98.4%; Score 1908; DB 2; Length 361;

Best Local Similarity 98.3%; Pred. No. 1.2e-140;

Matches 355; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

```

QY 1 MPPPKRRVQSKYVFLTYPCOSLSKEBALSQLQNLNTPVKKFKIKRELHENGEPHLAV 60
|
|
|
Db 1 MPPPKRRVQSKYVFLTYPCOSLSKEBALSQLQNLNTPVKKFKIKRELHENGEPHLAV 60
|
|
|
QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKGDITIEWGDPQIDG 120
|
|
|
Db 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKGDITIEWGDPQIDG 120
|
|
|
QY 121 RSARGGQOSANDSYAKALNAGSVOSALAVLREEQPKDFVLQNNHNRSLERIFAKAPEPW 180

```

```

Db 121 RSARGGQOSANDSYAKALNAGSVOSALAVLREEQPKDFVLQNNHNRSLERIFAKAPEPW 180
|
|
|
QY 181 VPPFQVSSFTNVPEDEQEMADNYFGTGDAAAPDRPVSIIYEGDSRTGKTMMARALGPHNY 240
|
|
|
Db 181 VPPFQVSSFTNVPEDEQEMADNYFGTGDAAAPDRPVSIIYEGDSRTGKTMMARALGPHNY 240
|
|
|
QY 241 LSGHLDNPGRVFNSNDVQYNYIDIDIAPHYLLKHKMKELLAGQKQWQSNCKTGKPVQIKGI 300
|
|
|
Db 241 LSGHLDNPGRVFNSNDVQYNYIDIDIAPHYLLKHKMKELLAGQKQWQSNCKTGKPVQIKGI 300
|
|
|
QY 301 PAIVLCNPGEGASKEFLDRAENTGLKNWTKKNAIFITLTPAPLYOESTQASOETGNQKQ 360
|
|
|
Db 301 PAIVLCNPGEGASKEFLDRAENTGLKNWTKKNAIFITLTPAPLYOESTQASOETGNQKQ 360
|
|
|
QY 361 G 361
|
|
|
Db 361 G 361

```

RESULT 3

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ID O71963 PRELIMINARY; PRT; 361 AA.
AC O71963;
DT 01-AUG-1998 (TREMBlrel. 07, Created)
DT 01-AUG-1998 (TREMBlrel. 07, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Replication associated protein.
GN Name=AC1;
OS Sida golden mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_Taxid=51034;
RN [1]
RP SEQUENCE FROM N.A.
RA Abouzid A.M., Polston J.E., Hiebert E.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
DR EMBL; AF049336; AAC05152.1; -.
DR HSSP; P27260; 1L5I.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001191; Gemin1 AL1.
DR InterPro; IPR001301; Gemin1 AL1_CLV.
DR Pfam; PF00799; Gemin1 AL1; 1.
DR PRINTS; PR00227; GEMCOATL1.
DR PRINTS; PR00228; GEMCOATL1.
DR ProDom; PD000736; Gemin1 AL1; 1.
SQ SEQUENCE 361 AA; 40678 MW; 57FA4DF1A86DD637 CRC64;

```

Query Match 92.4%; Score 1792; DB 2; Length 361;

Best Local Similarity 91.1%; Pred. No. 1.4e-131;

Matches 328; Conservative 20; Mismatches 12; Indels 0; Gaps 0;

```

QY 1 MPPPKRRVQSKYVFLTYPCOSLSKEBALSQLQNLNTPVKKFKIKRELHENGEPHLAV 60
|
|
|
Db 1 MPPPKRRVQSKYVFLTYPCOSLSKEBALSQLQNLNTPVKKFKIKRELHENGEPHLAV 60
|
|
|
QY 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKGDITIEWGDPQIDG 120
|
|
|
Db 61 LVQPEGKYQCTNNRFPDLVSPTRSAHFHPNIQAKSSDVKSYIDKGDITIEWGDPQIDG 120
|
|
|
QY 121 RSARGGQOSANDSYAKALNAGSVOSALAVLREEQPKDFVLQNNHNRSLERIFAKAPEPW 180
|
|
|
Db 121 RSARGGQOSANDSYAKALNAGSVOSALAVLREEQPKDFVLQNNHNRSLERIFAKAPEPW 180
|
|
|
QY 181 VPPFQVSSFTNVPEDEQEMADNYFGTGDAAAPDRPVSIIYEGDSRTGKTMMARALGPHNY 240
|
|
|
Db 181 VPPFQVSSFTNVPEDEQEMADNYFGTGDAAAPDRPVSIIYEGDSRTGKTMMARALGPHNY 240
|
|
|
QY 241 LSGHLDNPGRVFNSNDVQYNYIDIDIAPHYLLKHKMKELLAGQKQWQSNCKTGKPVQIKGI 300
|
|
|
Db 241 LSGHLDNPGRVFNSNDVQYNYIDIDIAPHYLLKHKMKELLAGQKQWQSNCKTGKPVQIKGI 300

```

QY 301 PAIVLCNPGSGASYKEFLDKAENTGLKNWTIKNAIFITTLAPLYOESTOASQETGNOKAQ 360
 DB 301 PAIVLCNPGSGASYKEFLDKAENTGLKNWTIKNAIFITTLAPLYOESTOASQEGHTEAR 360

RESULT 4

ID 011842 PRELIMINARY; PRT; 356 AA.
 AC 011842;
 DT 01-JUL-1997 (T-EMBLrel. 04, Created)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE 40.2 kDa.
 GN Name=ORF C1;
 OS Abutillon mosaic virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxId=10815;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91020984; PubMed=2219703;
 RA Frieschmuth T., Zimmat G., Jeske H.;
 RT "The nucleotide sequence of the abutillon mosaic virus reveals
 RT prokaryotic as well as eukaryotic features."
 RL Virology 178:461-468(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Jeske H.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
 DR EMBL: X15983; CAA34111.2; -;
 DR GO: GO:0019028; C: viral capsid; IEA.
 DR GO: GO:0005198; F: structural molecule activity; IEA.
 DR InterPro: IPR001191; Gemini AL1.
 DR Pfam: PF00799; Gemini AL1; I.
 DR PRINTS: PR00227; GEMCOATLVL.
 DR PRINTS: PR00228; GEMCOATLVL.
 DR ProDom: PD000736; Gemini AL1; 1.
 DR CHAIN 333 356 14.4 kDa.
 FT PRODOM: PD000736; Gemini AL1; 1.
 SQ SEQUENCE 356 AA; 40247 MW; 3AA732F65867352A CRC64;

Query Match 91.0%; Score 1764; DB 2; Length 356;
 Best Local Similarity 89.6%; Pred. No. 2.1e-129;
 Matches 319; Conservative 24; Mismatches 13; Indels 0; Gaps 0;

QY 1 MPPPKFRVQSKYKFLTYPCQSLSKKEBALSQLONTLPVNNKFKIKICREIHENGEPHLHY 60
 DB 1 MPPPKFRVQSKYKFLTYPCQSLSKKEBALSQLONTLPVNNKFKIKICREIHENGEPHLHY 60
 QY 61 LVQFEGKYQCTNNRPFDLVSPTRSAHFHPNIOGAKSSDVKSYIDKGDITIEWGDFQIDG 120
 DB 61 LVQFEGKYQCTNNRPFDLVSPTRSAHFHPNIOGAKSSDVKSYIDKGDITIEWGDFQIDG 120
 QY 121 RSRARGQOQSANDSYAALNAGSVOSALAVREOPKDFVLONHNIRSNLERIPAKAPEPW 180
 DB 121 RSRARGQOQSANDSYAALNAGSVOSALAVREOPKDFVLONHNIRSNLERIPAKAPEPW 180
 QY 181 VPPFOVSSFTNVVDENQEMADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTMMARALGPVNY 240
 DB 181 VPPFOVSSFTNVVDENQEMADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTMMARALGPVNY 240
 QY 241 LSGHLDPNRVPNDVQVNVYIDIAHYLKLKMKWKLGAQKQWQSNCKYKGRVQIKGGI 300
 DB 241 LSGHLDPNRVPNDVQVNVYIDIAHYLKLKMKWKLGAQKQWQSNCKYKGRVQIKGGI 300
 QY 301 PAIVLCNPGSGASYKEFLDKAENTGLKNWTIKNAIFITTLAPLYOESTOASQETGNOKAQ 356
 DB 301 PAIVLCNPGSGASYKEFLDKAENTGLKNWTIKNAIFITTLAPLYOESTOASQEGHTEAR 356

RESULT 5
 Q9YL74 PRELIMINARY; PRT; 361 AA.
 ID Q9YL74

AC Q9YL74;
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE AC1 protein.
 OS Chino del tomate virus-[IC].
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 OX NCBI_TaxId=22455;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Jiang H., Hou Y.-M., Guzman P., Gilbertson R.L.;
 RT "complete nucleotide sequence of the infectious clone of tomato leaf
 RT crumple geminivirus."
 RL (in) Unknown A. (eds.);
 RL ANNUAL MEETING OF THE AMERICAN PHYTOPATHOLOGICAL SOCIETY,
 RL PHYTOPATHOLOGY, VOL 88 (SUPPL), pp.44-0, Unknown publisher (1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Jiang H., Hou Y.-M., Guzman P., Gilbertson R.L.;
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
 DR EMBL: AF101476; AAD17898.1; -;
 DR HSSP: P27260; 1L51.
 DR GO: GO:0019028; C: viral capsid; IEA.
 DR GO: GO:0005198; F: structural molecule activity; IEA.
 DR InterPro: IPR001191; Gemini AL1.
 DR Pfam: PF00799; Gemini AL1; I.
 DR PRINTS: PR00227; GEMCOATLVL.
 DR PRINTS: PR00228; GEMCOATLVL.
 DR ProDom: PD000736; Gemini AL1; 1.
 SQ SEQUENCE 361 AA; 40826 MW; 7968527DD3A185B1 CRC64;

Query Match 89.5%; Score 1736; DB 2; Length 361;
 Best Local Similarity 88.3%; Pred. No. 3.3e-127;
 Matches 316; Conservative 25; Mismatches 17; Indels 0; Gaps 0;

QY 1 MPPPKFRVQSKYKFLTYPCQSLSKKEBALSQLONTLPVNNKFKIKICREIHENGEPHLHY 60
 DB 1 MPPPKFRVQSKYKFLTYPCQSLSKKEBALSQLONTLPVNNKFKIKICREIHENGEPHLHY 60
 QY 61 LVQFEGKYQCTNNRPFDLVSPTRSAHFHPNIOGAKSSDVKSYIDKGDITIEWGDFQIDG 120
 DB 61 LVQFEGKYQCTNNRPFDLVSPTRSAHFHPNIOGAKSSDVKSYIDKGDITIEWGDFQIDG 120
 QY 121 RSRARGQOQSANDSYAALNAGSVOSALAVREOPKDFVLONHNIRSNLERIPAKAPEPW 180
 DB 121 RSRARGQOQSANDSYAALNAGSVOSALAVREOPKDFVLONHNIRSNLERIPAKAPEPW 180
 QY 181 VPPFOVSSFTNVVDENQEMADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTMMARALGPVNY 240
 DB 181 VPPFOVSSFTNVVDENQEMADNYFGTGDAAAPPDRPVSIIVEGDSRTGKTMMARALGPVNY 240
 QY 241 LSGHLDPNRVPNDVQVNVYIDIAHYLKLKMKWKLGAQKQWQSNCKYKGRVQIKGGI 300
 DB 241 LSGHLDPNRVPNDVQVNVYIDIAHYLKLKMKWKLGAQKQWQSNCKYKGRVQIKGGI 300
 QY 301 PAIVLCNPGSGASYKEFLDKAENTGLKNWTIKNAIFITTLAPLYOESTOASQETGNOKAQ 358
 DB 301 PAIVLCNPGSGASYKEFLDKAENTGLKNWTIKNAIFITTLAPLYOESTOASQEGHTEAR 358

RESULT 6
 Q7THT9 PRELIMINARY; PRT; 361 AA.
 ID Q7THT9
 AC Q7THT9;
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Replicase.
 GN Name=AC1;
 OS Tomato mottle Taino virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.

NCBI_TaxID=223358;
 [1]
 RN SEQUENCE FROM N.A.
 RA Hernandez L.;
 RT "Caracterización molecular de geminivirus en papa (Solanum tuberosum L.)";
 RL Thesis (2000), Department of Biology, Universidad de La Habana, Ciudad de La Habana, Cuba.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Cordero M., Ramos P.L., Hernandez L., Fernandez A.I., Echemendia A.L., Peral R., Gonzalez G., Garcia D., Valdes S., Estevez A., Hernandez K.;
 RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ563919; CAD91703.1; -;
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR001191; Gemini_AL1.
 DR Pfam; PF00799; Gemini_AL1.
 DR Prodom; PD000736; Gemini_AL1.
 DR SEQUENCE 361 AA; 40735 MW; 78E289146A769404 CRC64;

Query Match 89.3%; Score 1731; DB 2; Length 361;
 Best Local Similarity 88.3%; Pred. No. 8e-127;
 Matches 316; Conservative 23; Mismatches 19; Indels 0; Gaps 0;

QY 1 MPPPKFRVQSKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKIKREIHENGEPHLHV 60
 DB 1 MPRKGSFSVAKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKIKREIHENGEPHLHV 60
 QY 61 LVQFEGKYCTNNRFFDLVPSPTSAHFHPIIQAKSSDVKSYIDKQDITLWGDIFQIDG 120
 DB 61 LVQFEGKYCTNNRFFDLVPSPTSAHFHPIIQAKSSDVKSYIDKQDITLWGDIFQIDG 120
 QY 121 RSRAGGQOSANDSYAKALNAGVQSALAVLREBPQDFVLQNNHNRSLERIFAKADEPW 180
 DB 121 RSRAGGQOSANDSYAKALNAGVQSALAVLREBPQDFVLQNNHNRSLERIFAKADEPW 180
 QY 121 RSRAGGQOSANDSYAKALNAGVQSALAVLREBPQDFVLQNNHNRSLERIFAKADEPW 180
 DB 121 RSRAGGQOSANDSYAKALNAGVQSALAVLREBPQDFVLQNNHNRSLERIFAKADEPW 180
 QY 181 VPPFOVSSFTNVDEMOEMADNYFGTDAAPPDPRVSIIVEGDSRTGKTMMARALGPHNY 240
 DB 181 VPPPLSSFTNVDEMOEMADNYFGAGSARPRPMSIVIEGDSRTGKTMMARALGPHNY 240
 QY 241 LSGHLDNNGVFNVDVQYNYIDIAPIHYLKLKMKKELGAKQWQSNCKYKGPQVIGKI 300
 DB 241 LSGHLDNNTVYNDVQYNYIDIAPIHYLKLKMKKELGAKQWQSNCKYKGPQVIGKI 300
 QY 301 PAIVLCNPGEGASKEFLDKAENTGLKNWTKNAIFITLPAPLYOESTQASQETGNOK 358
 DB 301 PAIVLCNPGEGASKDFLSKDENTSLRDWTKNAIFITLTPLYQDSTQARQEGNGE 358

RESULT 7

036624 PRELIMINARY; PRT; 361 AA.
 AC 036624;
 DT 01-JAN-1998 (TREMBlrel. 05, Created)
 DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Replication associated protein.
 OS Tomato mottle Taino virus.
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 NCBI_TaxID=223358;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Ramos P.L., Guerra O., Peral P., Oramas P., Guevara R.G., Rivera-Bustamante R.;
 RT "Taino tomato mottle virus, a new bipartite geminivirus from Cuba."; Plant Dis. 0:0-0(1997).
 CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
 DR EMBL; AF012300; AAO09668.1; -;
 DR HSSP; P27260; ILSI.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR001191; Gemini_AL1.

InterPro; IPR001301; Gemini_AL1_CLV.
 DR Pfam; PF00799; Gemini_AL1_I.
 DR PRINTS; PR00227; GEMCOATL1.
 DR PRINTS; PR00228; GEMCOATCVL1.
 DR Prodom; PD000736; Gemini_AL1.
 DR SEQUENCE 361 AA; 40722 MW; 3D43D231F8CC7FB5 CRC64;

Query Match 88.8%; Score 1722; DB 2; Length 361;
 Best Local Similarity 87.7%; Pred. No. 4.1e-126;
 Matches 314; Conservative 24; Mismatches 20; Indels 0; Gaps 0;

QY 1 MPPPKFRVQSKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKIKREIHENGEPHLHV 60
 DB 1 MPRKGSFSVAKNYFLTYPCQSLSKERALSQLQNLNTPVKKFKIKREIHENGEPHLHV 60
 QY 61 LVQFEGKYCTNNRFFDLVPSPTSAHFHPIIQAKSSDVKSYIDKQDITLWGDIFQIDG 120
 DB 61 LVQFEGKYCTNNRFFDLVPSPTSAHFHPIIQAKSSDVKSYIDKQDITLWGDIFQIDG 120
 QY 121 RSRAGGQOSANDSYAKALNAGVQSALAVLREBPQDFVLQNNHNRSLERIFAKADEPW 180
 DB 121 RSRAGGQOSANDSYAKALNAGVQSALAVLREBPQDFVLQNNHNRSLERIFAKADEPW 180
 QY 181 VPPFOVSSFTNVDEMOEMADNYFGTDAAPPDPRVSIIVEGDSRTGKTMMARALGPHNY 240
 DB 181 VPPPLSSFTNVDEMOEMADNYFGAGSARPRPMSIVIEGDSRTGKTMMARALGPHNY 240
 QY 241 LSGHLDNNGVFNVDVQYNYIDIAPIHYLKLKMKKELGAKQWQSNCKYKGPQVIGKI 300
 DB 241 LSGHLDNNTVYNDVQYNYIDIAPIHYLKLKMKKELGAKQWQSNCKYKGPQVIGKI 300
 QY 301 PAIVLCNPGEGASKEFLDKAENTGLKNWTKNAIFITLPAPLYOESTQASQETGNOK 358
 DB 301 PAIVLCNPGEGASKDFLSKDENTSLRDWTKNAIFITLTPLYQDSTQARQEGNGE 358

RESULT 8

093051 PRELIMINARY; PRT; 361 AA.
 AC 093051;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Replication initiator protein.
 GN Name=AC1;
 OS Chino del tomate virus-[88].
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
 NCBI_TaxID=222454;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Brown J.K., Nelson M.R.;
 RT "Transmission, host range, and virus-vector relationships of chino del tomate virus, a whitefly-transmitted geminivirus from Sinaloa, Mexico."; Plant Dis. 72:866-869(1988).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Brown J.K., Ostrow K.M., Idris A.M., Stenger D.C.;
 RT "Chino del tomate virus: relationships to other begomoviruses and the identification of A component variants that affect symptom expression."; Phytopathology 90:546-552(2000).
 CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
 DR EMBL; AF226664; AAF36703.1; -;
 DR HSSP; P27260; ILSI.
 DR GO; GO:0019028; C:Viral capsid; IEA.
 DR GO; GO:0005198; F:Structural molecule activity; IEA.
 DR InterPro; IPR001191; Gemini_AL1.
 DR InterPro; IPR001301; Gemini_AL1_CLV.
 DR Pfam; PF00799; Gemini_AL1_I.
 DR PRINTS; PR00227; GEMCOATL1.
 DR PRINTS; PR00228; GEMCOATCVL1.
 DR Prodom; PD000736; Gemini_AL1_I.

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SQ SEQUENCE 361 AA; 40970 MW; 9AF6F3865E1C2B822 CRC64;
Query Match 88.2%; Score 1715; DB 2; Length 361;
Best Local Similarity 87.2%; Pred. No. 1,4e-125;
Matches 312; Conservative 26; Mismatches 20; Indels 0; Gaps 0;

QY 1 MPPPKFVQAKNYFLTYPCQCSLSKEBALSQLONTLPVNNKFKIKICREIHENGEPHLHY 60
DB 1 MPPPKFVQAKNYFLTYPCQCSLSKEBALSQLONTLPVNNKFKIKICREIHENGEPHLHY 60
QY 61 LVDFEKGQCTNNRFPDLVSPTRSAHFHFNIOGAKSSDVKSYYIDXDGTIEMGDFOIDG 120
DB 61 LVDFEKGQCTNNRFPDLVSPTRSAHFHFNIOGAKSSDVKSYYIDXDGTIEMGDFOIDG 120
QY 121 RSARGGQQSANDSYAKALNAGSYQALAVLREBQPDVYLQNNINISNLERIPAKAPEPW 180
DB 121 RSARGGQQSANDSYAKALNAGSYQALAVLREBQPDVYLQNNINISNLERIPAKAPEPW 180
QY 181 VPPFQVSSFTNVDEQEWADNYFGTGDAAPPRPVSIIYEGSRGKTMMARALGPBNY 240
DB 181 VPPFQVSSFTNVDEQEWADNYFGTGDAAPPRPVSIIYEGSRGKTMMARALGPBNY 240
QY 241 LSGHLPNGRVFNSNDVQYNNVDDIAPHYKLKMKKELLSQKQWQSNCKYKGFVQIKGKI 300
DB 241 LSGHLPNGRVFNSNDVQYNNVDDIAPHYKLKMKKELLSQKQWQSNCKYKGFVQIKGKI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITTLTAPLYQSTOASQETGNQK 358
DB 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITTLTAPLYQSTOASQETGNQK 358
RESULT 9
Q96612 PRELIMINARY; PRT; 361 AA.
AC Q96612;
DT 01-FEB-1997 (TEMBLrel. 02, Created)
DT 01-FEB-1997 (TEMBLrel. 02, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE AC1 protein.
GN Name=AC1;
OS Abutilon mosaic virus-HW.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=222059;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Hawaii;
RA Wu Z.C., Hu J.S., Polston J.E., Ullman D.E., Hiebert E.;
RT "Complete nucleotide sequence of a non-vector transmissible strain of
abutilon mosaic geminivirus in Hawaii.";
RL Phytopathology 86:608-613 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Hawaii;
RA Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
EMBL: U51137; AAB18173.1; -.
DR HSSP: P27260; 1L5I.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR001191; Geminivirus.
DR InterPro: IPR001301; Geminivirus.
DR Pfam: PF00799; Geminivirus.
DR PRINTS: PR00227; GEMCOATL1.
DR PRINTS: PR00228; GEMCOATL1.
DR PRODOM: PD000736; Geminivirus.
SQ SEQUENCE 361 AA; 40886 MW; 034D5A7608253CDC CRC64;
Query Match 88.2%; Score 1711; DB 2; Length 361;
Best Local Similarity 86.9%; Pred. No. 2,9e-125;
Matches 313; Conservative 26; Mismatches 21; Indels 0; Gaps 0;
QY 1 MPPPKFVQAKNYFLTYPCQCSLSKEBALSQLONTLPVNNKFKIKICREIHENGEPHLHY 60
```

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DB 1 MPPPKFVQAKNYFLTYPCQCSLSKEBALSQLONTLPVNNKFKIKICREIHENGEPHLHY 60
QY 61 LVDFEKGQCTNNRFPDLVSPTRSAHFHFNIOGAKSSDVKSYYIDXDGTIEMGDFOIDG 120
DB 61 LVDFEKGQCTNNRFPDLVSPTRSAHFHFNIOGAKSSDVKSYYIDXDGTIEMGDFOIDG 120
QY 121 RSARGGQQSANDSYAKALNAGSYQALAVLREBQPDVYLQNNINISNLERIPAKAPEPW 180
DB 121 RSARGGQQSANDSYAKALNAGSYQALAVLREBQPDVYLQNNINISNLERIPAKAPEPW 180
QY 181 VPPFQVSSFTNVDEQEWADNYFGTGDAAPPRPVSIIYEGSRGKTMMARALGPBNY 240
DB 181 VPPFQVSSFTNVDEQEWADNYFGTGDAAPPRPVSIIYEGSRGKTMMARALGPBNY 240
QY 241 LSGHLPNGRVFNSNDVQYNNVDDIAPHYKLKMKKELLSQKQWQSNCKYKGFVQIKGKI 300
DB 241 LSGHLPNGRVFNSNDVQYNNVDDIAPHYKLKMKKELLSQKQWQSNCKYKGFVQIKGKI 300
QY 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITTLTAPLYQSTOASQETGNQK 360
DB 301 PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITTLTAPLYQSTOASQETGNQK 360
RESULT 10
Q9J049 PRELIMINARY; PRT; 361 AA.
AC Q9J049;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Replication initiator protein.
GN Name=AC1;
OS Chino del tomate virus-[H6].
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OX NCBI_TaxID=222453;
RN [1]
RP SEQUENCE FROM N.A.
RC Brown J.K., Nelson M.R.;
RA "Transmission, host range, and virus-vector relationships of chino del
tomate virus, a whitefly-transmitted geminivirus from Sinaloa,
Mexico.";
RL Plant Dis. 72:866-869 (1988).
RN [2]
RP SEQUENCE FROM N.A.
RC Brown J.K., Ostrow K.M., Idris A.M., Stenger D.C.;
RA "Chino del tomate virus: relationships to other begomoviruses and the
identification of A component variants that affect symptom
expression.";
RL Phytopathology 90:546-552 (2000).
CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
EMBL: AF226665; AAF36708.1; -.
DR HSSP: P27260; 1L5I.
DR GO: GO:0019028; C:viral capsid; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR001191; Geminivirus.
DR InterPro: IPR001301; Geminivirus.
DR Pfam: PF00799; Geminivirus.
DR PRINTS: PR00227; GEMCOATL1.
DR PRINTS: PR00228; GEMCOATL1.
DR PRODOM: PD000736; Geminivirus.
SQ SEQUENCE 361 AA; 40928 MW; 85B43340272ABE10 CRC64;
Query Match 88.2%; Score 1710; DB 2; Length 361;
Best Local Similarity 86.6%; Pred. No. 3,5e-125;
Matches 310; Conservative 27; Mismatches 21; Indels 0; Gaps 0;
QY 1 MPPPKFVQAKNYFLTYPCQCSLSKEBALSQLONTLPVNNKFKIKICREIHENGEPHLHY 60
DB 1 MPPPKFVQAKNYFLTYPCQCSLSKEBALSQLONTLPVNNKFKIKICREIHENGEPHLHY 60
QY 61 LVDFEKGQCTNNRFPDLVSPTRSAHFHFNIOGAKSSDVKSYYIDXDGTIEMGDFOIDG 120
DB 61 LVDFEKGQCTNNRFPDLVSPTRSAHFHFNIOGAKSSDVKSYYIDXDGTIEMGDFOIDG 120
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Db 61 LIQEGKYQCTNNRFPDLVSPTRSAHFHNPNIQGAKSSSDVKS YIDKDGDTIEMGEFQIDG 120
Qy 121 RSARGGQGSANDSYAKALNAGSVQSLAVIREOPKDFVQNNIRISNLERIPAKABEPW 180
Db 121 RSARGGQGSANDSYAKALNAGSVQSLAVIREOPKDFVQNNIRISNLERIPAKABEPW 180
Qy 181 VPPFOVSSFTNVDEDMQEMADNYFGTGDAAFPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
Db 181 VPPFOVSSFTNVDEDMQEMADNYFGTGDAAFPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
Qy 241 LSGHLDPNFNGRVFSDVQYNNVYIDIAPHYKLKHWKELLGAQKQWQSNCKYKGPVQIKGI 300
Db 241 LSGHLDPNFNGRVFSDVQYNNVYIDIAPHYKLKHWKELLGAQKQWQSNCKYKGPVQIKGI 300
Qy 301 PAIVLCNPGGAGASYKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQESTQASQETGNOK 358
Db 301 PAIVLCNPGGAGASYKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQESTQASQETGNOK 358
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RESULT 11

```
PRELIMINARY; PRT; 361 AA.
ID P89127
AC P89127;
DT 01-MAY-1997 (TEMBLrel. 03, Created)
DT 01-JAN-1998 (TEMBLrel. 05, Last sequence update)
DE 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE AC1 protein.
GN Name=AC1;
OS Sida yellow vein virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_Taxid=223321;
RX STRAIN=Honduras;
MEDLINE=98007646; Pubmed=9349490;
RA Frieschmuth T., Engel M., Lauster S., Jeske H.;
RT "Nucleotide sequence evidence for the occurrence of three distinct
RT whitefly-transmitted, Sida-infecting bipartite geminiviruses in
RT Central America.";
RL J. Gen. Virol. 78:2675-2682(1997).
CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
DR EMBL; Y11099; CAU71980.1; -.
DR HSSP; P27260; ILS1.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR001191; Gemin1_AL1_CTV.
DR Pfam; PF00799; Gemin1_AL1.
DR PRINTS; PR00227; GEMCOATL1.
DR PRINTS; PR00228; GEMCOATL1.
DR ProDom; PD000736; Gemin1_AL1.1.
SQ SEQUENCE 361 AA; 40956 MW; DF473608465F2987 CRC64;
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Query Match 87.2%; Score 1690; DB 2; Length 361;
Best Local Similarity 85.8%; Pred. No. 1.3e-123;
Matches 307; Conservative 26; Mismatches 25; Indels 0; Gaps 0;

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Qy 1 MPPPKKRVOSKNYFLTYPCSLSKERALSQLQNLNTPVVKKFKIKRELHENGEPRLHY 60
Db 1 MPPPKKRVOSKNYFLTYPCSLSKERALSQLQNLNTPVVKKFKIKRELHENGEPRLHY 60
Qy 61 LVQEGKYQCTNNRFPDLVSPTRSAHFHNPNIQGAKSSSDVKS YIDKDGDTIEMGEFQIDG 120
Db 61 LVQEGKYQCTNNRFPDLVSPTRSAHFHNPNIQGAKSSSDVKS YIDKDGDTIEMGEFQIDG 120
Qy 121 RSARGGQGSANDSYAKALNAGSVQSLAVIREOPKDFVQNNIRISNLERIPAKABEPW 180
Db 121 RSARGGQGSANDSYAKALNAGSVQSLAVIREOPKDFVQNNIRISNLERIPAKABEPW 180
Qy 181 VPPFOVSSFTNVDEDMQEMADNYFGTGDAAFPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
Db 181 VPPFOVSSFTNVDEDMQEMADNYFGTGDAAFPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
```

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Qy 241 LSGHLDPNFNGRVFSDVQYNNVYIDIAPHYKLKHWKELLGAQKQWQSNCKYKGPVQIKGI 300
Db 241 LSGHLDPNFNGRVFSDVQYNNVYIDIAPHYKLKHWKELLGAQKQWQSNCKYKGPVQIKGI 300
Qy 301 PAIVLCNPGGAGASYKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQESTQASQETGNOK 358
Db 301 PAIVLCNPGGAGASYKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQESTQASQETGNOK 358
```

RESULT 12

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PRELIMINARY; PRT; 361 AA.
ID Q8JUV1
AC Q8JUV1;
DT 01-OCT-2002 (TEMBLrel. 22, Created)
DT 01-OCT-2002 (TEMBLrel. 22, Last sequence update)
DE 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Replication associated protein.
GN Name=AC1;
OS Tobacco leaf rugose virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
NCBI_Taxid=196691;
RX SEQUENCE FROM N.A.
RA Dominguez M., Ramos P.L., Echemendia A.L., Crespo J., Peral R.,
RA Pujol M., Andino V., Borroto C.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
DR EMBL; AJ488768; CAD32806.1; -.
DR HSSP; P27260; ILS1.
DR GO; GO:0019028; C:Viral capsid; IEA.
DR GO; GO:0005198; F:Structural molecule activity; IEA.
DR InterPro; IPR001191; Gemin1_AL1.
DR Pfam; PF00799; Gemin1_AL1_CTV.
DR PRINTS; PR00227; GEMCOATL1.
DR PRINTS; PR00228; GEMCOATL1.
DR ProDom; PD000736; Gemin1_AL1.1.
SQ SEQUENCE 361 AA; 41036 MW; 1291C2DC119EABAI CRC64;
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Query Match 87.1%; Score 1689; DB 2; Length 361;
Best Local Similarity 86.1%; Pred. No. 1.5e-123;
Matches 311; Conservative 24; Mismatches 24; Indels 2; Gaps 2;

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Qy 1 MPPPKKRVOSKNYFLTYPCSLSKERALSQLQNLNTPVVKKFKIKRELHENGEPRLHY 60
Db 1 MPPPKKRVOSKNYFLTYPCSLSKERALSQLQNLNTPVVKKFKIKRELHENGEPRLHY 60
Qy 61 LVQEGKYQCTNNRFPDLVSPTRSAHFHNPNIQGAKSSSDVKS YIDKDGDTIEMGEFQIDG 120
Db 61 LVQEGKYQCTNNRFPDLVSPTRSAHFHNPNIQGAKSSSDVKS YIDKDGDTIEMGEFQIDG 120
Qy 121 RSARGGQGSANDSYAKALNAGSVQSLAVIREOPKDFVQNNIRISNLERIPAKABEPW 180
Db 121 RSARGGQGSANDSYAKALNAGSVQSLAVIREOPKDFVQNNIRISNLERIPAKABEPW 180
Qy 181 VPPFOVSSFTNVDEDMQEMADNYFGTGDAAFPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
Db 181 VPPFOVSSFTNVDEDMQEMADNYFGTGDAAFPDRPVSIIVEGDSRTGKTMMARALGPHNY 240
Qy 241 LSGHLDPNFNGRVFSDVQYNNVYIDIAPHYKLKHWKELLGAQKQWQSNCKYKGPVQIKGI 300
Db 241 LSGHLDPNFNGRVFSDVQYNNVYIDIAPHYKLKHWKELLGAQKQWQSNCKYKGPVQIKGI 300
Qy 301 PAIVLCNPGGAGASYKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQESTQASQETGNOK 359
Db 301 PAIVLCNPGGAGASYKEFLDKAENTGLKNWTTIKNAIFITLTAPLYQESTQASQETGNOK 359
```

RESULT 13

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Q67558
ID O67558 PRELIMINARY; PRT; 361 AA.
AC O67558;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Replicative protein.
GN Name=AL1;
OS Bean dwarf mosaic virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxId=10838;
RN [1]
RP SEQUENCE FROM N.A.
RA Gilbertson R.L., Faria J.C., Hanson S.F., Morales F.J., Ahlquist P.G.,
RA Maxwell D.P., Russell D.R.;
RT "Cloning of the complete DNA genomes of four bean-infecting
RT geminiviruses and determining their infectivity by electric discharge
RT particle acceleration.";
RL Phycopathology 81:980-985(1991).
[2]
RN [2]
RP SEQUENCE FROM N.A.
RA Hidayat S.H., Gilbertson R.L., Hanson S.F., Morales F.J.,
RA Ahlquist P.G., Russell D.R., Maxwell D.P.;
RL Submitted (May-1992) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
DR EMBL; M88179; AAC32402.1; -.
DR HSSP; P27260; 1L5I.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001191; Gemin1_AL1.
DR InterPro; IPR001301; Gemin1_AL1_CLV.
DR Pfam; PF00799; Gemin1_AL1.
DR PRINTS; PR00227; GEMCOATL1.
DR PRINTS; PR00228; GEMCOATL1.
DR ProDom; PD000736; Gemin1_AL1.
SQ SEQUENCE 361 AA; 40733 MW; A26939B1BEF923A8 CRC64;

Query Match 85.8%; Score 1664; DB 2; Length 361;
Best Local Similarity 83.2%; Pred. No. 1.4e-121;
Matches 298; Conservative 35; Mismatches 25; Indels 0; Gaps 0;

QY 1 MPBPKKPRVQSKNYFLTPQCSLSKEBALSQLQNLNTPVNNKFKICRELEHNGEPHLAV 60
DB 1 MPBPKKPRVQSKNYFLTPQCSLSKEBALSQLQNLNTPVNNKFKICRELEHNGEPHLAV 60
QY 61 LVOPEGKYQCTNNRPFPLVSPTRSAHFHPNIQGAKSSSDVKSVIDKDGDTIEWGDFQIDG 120
DB 61 LVOPEGKYQCTNNRPFPLVSPTRSAHFHPNIQGAKSSSDVKSVIDKDGDTIEWGDFQIDG 120
QY 61 LIQFEGKYQCTNNRPFPLVSPTRSAHFHPNIQGAKSSSDVKSVIDKDGDTIEWGDFQIDG 120
DB 61 LIQFEGKYQCTNNRPFPLVSPTRSAHFHPNIQGAKSSSDVKSVIDKDGDTIEWGDFQIDG 120
QY 121 RSARGGQGSANDSYAKALNAGSVALVIREOPKDFVLQNNHNSLERTFAKAPBPW 180
DB 121 RSARGGQGSANDSYAKALNAGSVALVIREOPKDFVLQNNHNSLERTFAKAPBPW 180
QY 121 RSARGGQGSANDSYAKALNAGSVALVIREOPKDFVLQNNHNSLERTFAKAPBPW 180
DB 121 RSARGGQGSANDSYAKALNAGSVALVIREOPKDFVLQNNHNSLERTFAKAPBPW 180
QY 181 VPFQVSSFTNVPEMQEADNYFCGTDAAPDRPVSIIVEGDSRTGKTMARALGPHNYL 240
DB 181 VPFQVSSFTNVPEMQEADNYFCGTDAAPDRPVSIIVEGDSRTGKTMARALGPHNYL 240
QY 181 VPFQVSSFTNVPEMQEADNYFCGTDAAPDRPVSIIVEGDSRTGKTMARALGPHNYL 240
DB 181 VPFQVSSFTNVPEMQEADNYFCGTDAAPDRPVSIIVEGDSRTGKTMARALGPHNYL 240
QY 241 LSGHLDPNRGNVSNVQYNYIDIDIAHYLKLKHWKELIGAQKQWQSNCKYGGKPVQIKGCI 300
DB 241 LSGHLDPNRGNVSNVQYNYIDIDIAHYLKLKHWKELIGAQKQWQSNCKYGGKPVQIKGCI 300
QY 241 LSGHLDPNRGNVSNVQYNYIDIDIAHYLKLKHWKELIGAQKQWQSNCKYGGKPVQIKGCI 300
DB 241 LSGHLDPNRGNVSNVQYNYIDIDIAHYLKLKHWKELIGAQKQWQSNCKYGGKPVQIKGCI 300
QY 301 PAIVLCPGEGASKEFLDKAENTGLKNWTKIKNAIFITLTAPLYOESTQASOETGNOK 358
DB 301 PAIVLCPGEGASKEFLDKAENTGLKNWTKIKNAIFITLTAPLYOESTQASOETGNOK 358
QY 301 PAIVLCPGEGASKEFLDKAENTGLKNWTKIKNAIFITLTAPLYOESTQASOETGNOK 358
DB 301 PAIVLCPGEGASKEFLDKAENTGLKNWTKIKNAIFITLTAPLYOESTQASOETGNOK 358

RESULT 14
ID O71205 PRELIMINARY; PRT; 350 AA.
AC O71205;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
```

```
DE Replication-associated protein.
GN Name=AC1;
OS Potato yellow mosaic Trinidad virus [Trinidad & Tobago].
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxId=223109;
RN [1]
RP SEQUENCE FROM N.A.
RA Humaharan P., Padidam M., Phelps R.H., Beachy R.N., Fauquet C.M.;
RA Submitted (DEC-1997) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
DR EMBL; AF039031; AAC09254.1; -.
DR HSSP; P27260; 1L5I.
DR GO; GO:0019028; C:viral capsid; IEA.
DR GO; GO:0005198; F:structural molecule activity; IEA.
DR InterPro; IPR001191; Gemin1_AL1.
DR InterPro; IPR001301; Gemin1_AL1_CLV.
DR Pfam; PF00799; Gemin1_AL1.
DR PRINTS; PR00227; GEMCOATL1.
DR PRINTS; PR00228; GEMCOATL1.
DR ProDom; PD000736; Gemin1_AL1.
SQ SEQUENCE 350 AA; 39567 MW; A08B3B3BFA1A068FD CRC64;

Query Match 85.2%; Score 1652; DB 2; Length 350;
Best Local Similarity 84.5%; Pred. No. 1.1e-120;
Matches 295; Conservative 27; Mismatches 27; Indels 0; Gaps 0;

QY 3 PPBPFRVQSKNYFLTPQCSLSKEBALSQLQNLNTPVNNKFKICRELEHNGEPHLAV 62
DB 2 PPBPFRVQSKNYFLTPQCSLSKEBALSQLQNLNTPVNNKFKICRELEHNGEPHLAV 61
QY 63 QFEGKYQCTNNRPFPLVSPTRSAHFHPNIQGAKSSSDVKSVIDKDGDTIEWGDFQIDG 122
DB 62 QFEGKYQCTNNRPFPLVSPTRSAHFHPNIQGAKSSSDVKSVIDKDGDTIEWGDFQIDG 121
QY 123 ARGGQGSANDSYAKALNAGSVALVIREOPKDFVLQNNHNSLERTFAKAPBPW 182
DB 122 ARGGQGSANDSYAKALNAGSVALVIREOPKDFVLQNNHNSLERTFAKAPBPW 181
QY 183 PFOVSSFTNVPEMQEADNYFCGTDAAPDRPVSIIVEGDSRTGKTMARALGPHNYL 242
DB 182 PFOVSSFTNVPEMQEADNYFCGTDAAPDRPVSIIVEGDSRTGKTMARALGPHNYL 241
QY 243 GHLDPNRGNVSNVQYNYIDIDIAHYLKLKHWKELIGAQKQWQSNCKYGGKPVQIKGCI 302
DB 242 GHLDPNRGNVSNVQYNYIDIDIAHYLKLKHWKELIGAQKQWQSNCKYGGKPVQIKGCI 301
QY 303 IVLCNPGEGASKEFLDKAENTGLKNWTKIKNAIFITLTAPLYOESTQAS 351
DB 302 IVLCNPGEGASKEFLDKAENTGLKNWTKIKNAIFITLTAPLYOESTQAS 350

RESULT 15
ID P89122 PRELIMINARY; PRT; 361 AA.
AC P89122;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE AC1 protein.
GN Name=AC1;
OS Sida golden mosaic Honduras virus.
OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.
OC NCBI_TaxId=223116;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=Honduras;
RA MEDLINE=98007646; PubMed=9349490;
RA Frischmuth T., Engel M., Lauster S., Jeske H.;
RT "Nucleotide sequence evidence for the occurrence of three distinct
RT whitefly-transmitted, Sida-infecting bipartite geminiviruses in
RT Central America.";
RL J. Gen. Virol. 78:2675-2682(1997).
```

CC -1- SIMILARITY: Belongs to the geminiviruses AL1 protein family.
DR EMBL: Y11097; CAA71973.1; -.
DR HSSP: P27260; 1LSI.
DR GO: GO:0019028; C:Viral capsid; IEA.
DR GO: GO:0005198; F:structural molecule activity; IEA.
DR InterPro: IPR001191; Gemini_AL1.
DR InterPro: IPR001301; Gemini_AL1_CLV.
DR Pfam: PF00799; Gemini_AL1; I.
DR PRINTS: PR00227; GEMCOATL1.
DR PRINTS: PR00228; GEMCOATL1.
DR PRODOM: PD000736; Gemini_AL1; I.
DR SEQUENCE 361 AA; 41137 MW; 5BE4C17CE1C7E4DF CRC64;

Query March 84.6% Score 1640; DB 2; Length 361;

Best Local Similarity 82.7%; Pred. No. 1e-119; Mismatches 33; Indels 0; Gaps 0;

Matches 296; Conservative 29; Mismatches 33; Indels 0; Gaps 0;

QY	1	MPPPKFRVVSQNYFLTYPOCSLSKEBALSQLQNLNTPVNNKFTIKICRELHENGEPHLHV	60
DB	1	MPPPKFRVVSQNYFLTYPOCSLTKEALSQLQNLNTPVNNKFTIKISRDKHENGEPHGHV	60
QY	61	LVOPEGKYOCCTNNRFFPLVSTPSRAHHPNIOGAKSSDVKSITDKDGTIEWGDFQIDG	120
DB	61	LIOPEGKYOCCTNNRFFPLVSTPSRSVHPNIOGAKSSDVKSITDKDGTIEWGQFQIDG	120
QY	121	RSARGGQOSANDSYAKALNAGSVOSALAVLREEQPKDFVLQNHNRSLERIFAKADEPW	180
DB	121	RSARGGQOTANDTYAKALNATCAEALRIIREGQPHFLQHNVLVANATKIFQKADPEW	180
QY	181	VPPQVSSFTNVPEMOEMADNYPGTDAAPDRPVSIIVEGDSRTGKTMMARALGPHNY	240
DB	181	APPEPLSSFTNVPEMOEMADEYFGRGAARPDPRMSLIIVEGDSRTGKTMMARALGPHNY	240
QY	241	LSGHLDFNGRVSNDVQYNYVDIAPHYLKLKHWKELLGAQKWQSNCKYGPVQIKGI	300
DB	241	LSGHLDFNPRVSNVEYNYVDVAPHYLKLKHWKELLGAQKWQSNCKYGPVQIKGI	300
QY	301	PAIVLCNPGEGASYKEFLDKAENTGLKNWTIKNAIFITLTAPLYQESTQASQETGNOK	358
DB	301	PSIVLCNPGEGASYKDFLDKEENASLKNWTIKNAIFITLTALYQDSTQASQEEVHOE	358

Search completed: December 3, 2004, 15:00:48
Job time : 195 secs